

Score over length search

ACCESS DB #

184133

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Scientific and Technical Information Center

## SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 4/4/06  
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 101643,038  
Location (Bldg/Room#): 2d28 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

\*\*\*\*\*

Ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: AS modr of h. PLA<sub>2</sub>, growth A

Inventors (please provide full names): Bennett et al

Earliest Priority Date: 5-25-01

### Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No: 17

between bases 994 - 1070 only

between

• Size limit to 8-50 Nucleobases

• Score over length search

• No interference please

~~Ther~~

• 70% Identity or greater

17-1080 na

Ther

EST-8  
ge-182  
ISS-100  
nqa 299  
pubmain 119  
pubnew 351

1d2  
BDB

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## SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70% , *length 8-50 nt*

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 16:13:31 ; Search time 0.001 Seconds  
(without alignments)  
334.488 Million cell updates/sec

Title: US-10-643-038-17\_994-1070

Perfect score: 77  
Sequence: 1 caaacaagacgctgggga.....gaagctgatctgtcaag 77

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 119 seqs, 2172 residues

Total number of hits satisfying chosen parameters: 238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 119 summaries

Database : pubmaindb.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	25	32.5	25	1	US-10-956-157-18260, A
2	25	32.5	25	1	US-10-956-157-157048
3	25	32.5	25	1	US-10-956-157-169708
4	25	32.5	25	1	US-11-060-756-94739
5	25	32.5	25	1	US-11-060-756-94763
6	24	31.2	25	1	US-10-956-157-150028
7	22	28.6	25	1	US-10-956-157-170149
8	21	27.3	25	1	US-10-956-157-141304
9	21	27.3	25	1	US-10-956-157-160508
10	21	27.3	25	1	US-11-060-756-152285
11	20	26.0	20	1	US-09-865-866-19
12	20	26.0	20	1	US-09-865-866-21
13	20	26.0	20	1	US-09-865-866-22
14	20	26.0	20	1	US-09-865-866-23
15	20	26.0	20	1	US-09-865-866-24
16	20	26.0	20	1	US-09-865-866-25
17	20	26.0	20	1	US-10-643-038-19
18	20	26.0	20	1	US-10-643-038-20
19	20	26.0	20	1	US-10-643-038-21
20	20	26.0	20	1	US-10-643-038-22
21	20	26.0	20	1	US-10-643-038-23
22	20	26.0	20	1	US-10-643-038-24
23	20	26.0	20	1	US-10-643-038-25
24	20	26.0	20	1	US-10-847-918-6072
25	17.8	23.1	21	1	US-11-036-317-81949
26	17.8	23.1	25	1	US-11-036-317-589182
27	17.8	23.1	25	1	US-10-719-956-632892
28	17.6	22.9	25	1	US-10-719-900-154278
29	17.6	22.9	25	1	US-10-719-900-338409
30	17.6	22.9	25	1	US-10-422-475-4
31	17	22.1	20	1	US-10-422-475-4
32	16.8	21.8	21	1	US-10-847-918-5566
33	16.8	21.8	21	1	US-10-847-918-5568

34	16.8	21.8	21	1	US-10-847-918-6070	Sequence 6070, Ap
35	16.4	21.3	21	1	US-10-847-918-5567	Sequence 5567, Ap
36	16.4	21.3	21	1	US-10-847-918-5569	Sequence 5569, Ap
c 37	16.4	21.3	21	1	US-10-847-918-5571	Sequence 5571, Ap
38	16.4	21.3	21	1	US-10-847-918-6071	Sequence 6071, Ap
39	15.4	20.0	21	1	US-10-847-918-5570	Sequence 5570, Ap
40	15.4	20.0	22	1	US-10-509-738-15	Sequence 15, Appl
c 41	15.2	19.7	21	1	US-10-751-736-9539	Sequence 9539, Ap
c 42	14.8	19.2	21	1	US-10-751-736-16743	Sequence 16743, A
c 43	14.8	19.2	21	1	US-10-751-736-17280	Sequence 17280, A
c 44	14.8	19.2	21	1	US-10-679-366-14	Sequence 14, Appl
c 45	14.8	19.2	21	1	US-10-847-918-5564	Sequence 5564, Ap
46	14.4	18.7	17	1	US-09-866-108-10026	Sequence 10026, A
47	14.4	18.7	17	1	US-09-866-108-10027	Sequence 10027, A
48	14.4	18.7	17	1	US-10-723-361-10026	Sequence 10026, A
49	14.4	18.7	17	1	US-10-723-361-10027	Sequence 10027, A
50	14	18.2	17	1	US-09-866-108-10024	Sequence 10024, A
51	14	18.2	17	1	US-09-866-108-10025	Sequence 10025, A
52	14	18.2	17	1	US-10-723-361-10024	Sequence 10024, A
53	14	18.2	17	1	US-10-723-361-10025	Sequence 10025, A
c 54	13.8	17.9	17	1	US-09-866-998-930	Sequence 930, App
c 55	13.4	17.4	17	1	US-09-866-108-10028	Sequence 10028, A
c 56	13.4	17.4	17	1	US-10-060-998-931	Sequence 931, App
c 57	13.4	17.4	17	1	US-10-060-998-932	Sequence 932, App
58	13.4	17.4	17	1	US-10-723-361-10028	Sequence 932, App
c 59	13.2	17.1	18	1	US-09-776-191-56	Sequence 56, Appl
c 60	13.2	17.1	18	1	US-10-092-004A-6	Sequence 6, Appl
61	13	16.9	17	1	US-09-866-108-10023	Sequence 10023, A
62	13	16.9	17	1	US-10-723-361-10023	Sequence 10023, A
c 63	13	16.9	18	1	US-10-367-980A-11	Sequence 11, Appl
c 64	12.8	16.6	17	1	US-10-060-998-929	Sequence 929, App
65	12.8	16.6	18	1	US-10-469-277-7	Sequence 7, Appl
66	12.4	16.1	17	1	US-09-866-108-10029	Sequence 10029, A
67	12.4	16.1	17	1	US-09-825-805-816	Sequence 816, App
c 68	12.4	16.1	17	1	US-10-060-998-927	Sequence 927, App
c 69	12.4	16.1	17	1	US-10-060-998-928	Sequence 928, App
c 70	12.4	16.1	17	1	US-10-060-998-933	Sequence 933, App
71	12.4	16.1	17	1	US-10-163-552-786	Sequence 786, App
72	12.4	16.1	17	1	US-10-138-674-7914	Sequence 7914, Ap
73	12.4	16.1	17	1	US-10-287-949A-7914	Sequence 7914, Ap
74	12.4	16.1	17	1	US-10-723-361-10029	Sequence 10029, A
75	12.4	16.1	17	1	US-10-712-633-1056	Sequence 1056, Ap
76	12.4	16.1	17	1	US-10-724-270-5441	Sequence 5441, Ap
c 77	12.2	15.8	17	1	US-09-864-785-2825	Sequence 2825, Ap
c 78	12.2	15.8	17	1	US-09-930-423-1056	Sequence 1056, Ap
79	12.2	15.8	17	1	US-09-745-237A-1056	Sequence 1056, Ap
c 80	12.2	15.8	17	1	US-10-138-674-8872	Sequence 8872, Ap
c 81	12.2	15.8	17	1	US-10-287-949A-8872	Sequence 8872, Ap
c 82	12.2	15.8	17	1	US-10-712-633-4058	Sequence 4058, Ap
83	12.2	15.8	17	1	US-10-913-280-108	Sequence 108, App
84	12	15.6	16	1	US-10-776-934-113	Sequence 113, App
85	12	15.6	16	1	US-10-776-934-592	Sequence 592, App
86	12	15.6	16	1	US-10-776-934-593	Sequence 593, App
87	12	15.6	16	1	US-10-776-934-594	Sequence 594, App
88	12	15.6	16	1	US-10-776-934-595	Sequence 595, App
89	12	15.6	17	1	US-09-866-108-10022	Sequence 10022, A
90	12	15.6	17	1	US-10-723-361-10022	Sequence 10022, A
c 91	11.8	15.3	16	1	US-10-138-674-6986	Sequence 6986, Ap
c 92	11.8	15.3	16	1	US-10-287-949A-6986	Sequence 6986, Ap
c 93	11.8	15.3	16	1	US-10-741-600-73537	Sequence 73537, A
c 94	11.4	14.8	13	1	US-10-257-0178-41787	Sequence 41787, A
c 95	11.4	14.8	13	1	US-10-257-0178-41788	Sequence 41788, A
c 96	11.4	14.8	13	1	US-10-257-0178-18441	Sequence 18441, A
c 97	11.4	14.8	13	1	US-10-257-0178-18442	Sequence 18442, A
c 98	11.4	14.8	16	1	US-10-142-729-26	Sequence 26, Appl
c 99	11.4	14.8	16	1	US-10-142-729-39	Sequence 39, Appl
c 100	11.4	14.8	16	1	US-10-375-504-26	Sequence 26, Appl
c 101	11.4	14.8	16	1	US-10-375-504-39	Sequence 39, Appl
c 102	11.4	14.8	16	1	US-10-719-993-55182	Sequence 55182, A
c 103	11.2	14.5	16	1	US-09-875-453-65	Sequence 65, Appl
c 104	11.2	14.5	16	1	US-10-331-907-450	Sequence 450, App
c 105	11.2	14.5	16	1	US-10-407-807-67	Sequence 67, Appl
c 106	11	14.3	11	1	US-10-450-797-548	Sequence 548, App

c 107 11 14.3 12 1 US-10-257-017B-320928 Sequence 320928,  
c 108 11 14.3 13 1 US-10-257-017B-14593 Sequence 14593, A  
c 109 11 14.3 13 1 US-10-257-017B-14594 Sequence 14594, A  
c 110 11 14.3 13 1 US-10-257-017B-181997 Sequence 181997,  
c 111 11 14.3 13 1 US-10-257-017B-181998 Sequence 181998,  
c 112 11 14.3 13 1 US-10-257-017B-224917 Sequence 224917,  
c 113 11 14.3 13 1 US-10-257-017B-224918 Sequence 224918,  
c 114 11 14.3 14 1 US-09-998-027-20 Sequence 20, Appl  
c 115 11 14.3 14 1 US-10-165-099-20 Sequence 20, Appl  
c 116 11 14.3 15 1 US-09-504-231A-1178 Sequence 1178, Ap  
c 117 11 14.3 15 1 US-09-504-231A-1179 Sequence 1179, Ap  
c 118 11 14.3 15 1 US-09-274-553D-1178 Sequence 1178, Ap  
c 119 11 14.3 15 1 US-09-274-553D-1179 Sequence 1179, Ap

## ALIGNMENTS

RESULT 1  
US-10-956-157-18260  
; Sequence 18260, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18260  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-18260

Query Match 32.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GATACAACTCTGGAGTCTCTGAGA 43  
|||||  
Db 1 GATACAACTCTGGAGTCTCTGAGA 25

RESULT 2  
US-10-956-157-157048  
; Sequence 157048, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 157048  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-157048

Query Match 32.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AACACAGCGCCTGGGATCAACT 27  
|||||

Db 1 AACACAGCGCCTGGGATCAACT 25  
RESULT 3  
US-10-956-157-169708  
; Sequence 169708, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 169708  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-169708

Query Match 32.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAAGACGGCCTGGGATCAACTCT 29  
|||||  
Db 1 CAAGACGGCCTGGGATCAACTCT 25

RESULT 4  
US-11-060-756-94739  
; Sequence 94739, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 94739  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-94739

Query Match 32.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GATACAACTCTGGAGTCTCTGAGA 43  
|||||  
Db 1 GATACAACTCTGGAGTCTCTGAGA 25

RESULT 5  
US-11-060-756-94763  
; Sequence 94763, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT FILING DATE: 2005-02-18

; NUMBER OF SEQ ID NOS: 303284  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 94763  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: probe  
 US-11-060-756-94763

Query Match 32.5%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGTCTCTGAG 42  
 |||||  
 Db 1 GGATACAACTCTGGAGTCTCTGAG 25

## RESULT 6

US-10-956-157-150028  
 ; Sequence 150028, Application US/10956157  
 ; Publication No. US20050118625A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William  
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
 ; FILE REFERENCE: 031896-043000 (AM 101081)  
 ; CURRENT APPLICATION NUMBER: US/10/956.157  
 ; CURRENT FILING DATE: 2004-10-04  
 ; NUMBER OF SEQ ID NOS: 319805  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 150028  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Probe Sequence  
 US-10-956-157-150028

Query Match 31.2%; Score 24; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 4.1;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAACAGACGGCTGGGATACA 24  
 |||||  
 Db 2 CAAACAGACGGCTGGGATACA 25

## RESULT 7

US-10-956-157-170149  
 ; Sequence 170149, Application US/10956157  
 ; Publication No. US20050118625A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William  
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
 ; FILE REFERENCE: 031896-043000 (AM 101081)  
 ; CURRENT APPLICATION NUMBER: US/10/956.157  
 ; CURRENT FILING DATE: 2004-10-04  
 ; NUMBER OF SEQ ID NOS: 319805  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 170149  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Probe Sequence  
 US-10-956-157-170149

Query Match 28.6%; Score 22; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 7.2;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CAACTCTGGAGTCTCTGAGAG 44  
 |||||  
 Db 1 CAACTCTGGAGTCTCTGAGAG 22

## RESULT 8

US-10-956-157-141304  
 ; Sequence 141304, Application US/10956157  
 ; Publication No. US20050118625A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William  
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
 ; FILE REFERENCE: 031896-043000 (AM 101081)  
 ; CURRENT APPLICATION NUMBER: US/10/956.157  
 ; CURRENT FILING DATE: 2004-10-04  
 ; NUMBER OF SEQ ID NOS: 319805  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 141304  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Probe Sequence  
 US-10-956-157-141304

Query Match 27.3%; Score 21; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 9.6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAACAGACGGCTGGGAT 21  
 |||||  
 Db 5 CAAACAGACGGCTGGGAT 25

## RESULT 9

US-10-956-157-160508  
 ; Sequence 160508, Application US/10956157  
 ; Publication No. US20050118625A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William  
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
 ; FILE REFERENCE: 031896-043000 (AM 101081)  
 ; CURRENT APPLICATION NUMBER: US/10/956.157  
 ; CURRENT FILING DATE: 2004-10-04  
 ; NUMBER OF SEQ ID NOS: 319805  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 160508  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Probe Sequence  
 US-10-956-157-160508

Query Match 27.3%; Score 21; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 9.6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 AACTCTGGAGTCTCTGAGAG 44  
 |||||  
 Db 1 AACTCTGGAGTCTCTGAGAG 21

## RESULT 10

US-11-060-756-152285  
 ; Sequence 152285, Application US/11060756  
 ; Publication No. US20050221354A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William Martin  
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
 ; FILE REFERENCE: AM101083 (031896-042000)  
 ; CURRENT APPLICATION NUMBER: US/11/060.756  
 ; CURRENT FILING DATE: 2005-02-18  
 ; NUMBER OF SEQ ID NOS: 303284

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 152285  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-152285

Query Match 27.3%; Score 21; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 AACTCTGGAGTCTCTGAGAG 44  
|||||  
Db 1 AACTCTGGAGTCTCTGAGAG 21  
|||||

RESULT 11  
US-09-865-866-19/c  
; Sequence 19, Application US/09865866  
; Publication No. US20030045487A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX  
; FILE REFERENCE: RTS-0221  
; CURRENT APPLICATION NUMBER: US/09/865,866  
; CURRENT FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 173  
; SEQ ID NO 19  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-865-866-19

Query Match 26.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACACAGACGGCTGGGGA 20  
|||||  
Db 20 CAACACAGACGGCTGGGGA 1  
|||||

RESULT 12  
US-09-865-866-20/c  
; Sequence 20, Application US/09865866  
; Publication No. US20030045487A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX  
; FILE REFERENCE: RTS-0221  
; CURRENT APPLICATION NUMBER: US/09/865,866  
; CURRENT FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 173  
; SEQ ID NO 20  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-865-866-20

Query Match 26.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCTGGGGATACAACTCTGG 31  
|||||  
Db 20 GCCTGGGGATACAACTCTGG 1  
|||||

RESULT 13  
US-09-865-866-21/c  
; Sequence 21, Application US/09865866  
; Publication No. US20030045487A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX  
; FILE REFERENCE: RTS-0221  
; CURRENT APPLICATION NUMBER: US/09/865,866  
; CURRENT FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 173  
; SEQ ID NO 21  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-865-866-21

Query Match 26.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCTCTGAG 42  
|||||  
Db 20 CAACTCTGGAGTCTCTGAG 1  
|||||

RESULT 14  
US-09-865-866-22/c  
; Sequence 22, Application US/09865866  
; Publication No. US20030045487A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX  
; FILE REFERENCE: RTS-0221  
; CURRENT APPLICATION NUMBER: US/09/865,866  
; CURRENT FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 173  
; SEQ ID NO 22  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-865-866-22

Query Match 26.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTCCTCTGAGAGGTAAGAG 52  
|||||  
Db 20 GTCCTCTGAGAGGTAAGAG 1  
|||||

RESULT 15  
US-09-865-866-23/c  
; Sequence 23, Application US/09865866  
; Publication No. US20030045487A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX  
; FILE REFERENCE: RTS-0221  
; CURRENT APPLICATION NUMBER: US/09/865,866  
; CURRENT FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 173  
; SEQ ID NO 23  
; LENGTH: 20

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-23

Query Match      26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 CTCGAGAGGTTAAAGAGCCA 55
Db 20 CTCGAGAGGTTAAAGAGCCA 1

RESULT 16
US-09-865-866-24/c
; Sequence 24, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RFS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-24

Query Match      26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AGAGGTTAAAGAGCCAGCGAA 60
Db 20 AGAGGTTAAAGAGCCAGCGAA 1

RESULT 17
US-09-865-866-25/c
; Sequence 25, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RFS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-25

Query Match      26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGTCCTGTCAAG 77
Db 20 GAAGCTGATGTCCTGTCAAG 1
```

```
RESULT 18
US-10-643-038-19/c
; Sequence 19, Application US/10643038
; Publication No. US2005014331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RFS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-038-19

Query Match      26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAACAGACGGCTGGGA 20
Db 20 CAAACAGACGGCTGGGA 1

RESULT 19
US-10-643-038-20/c
; Sequence 20, Application US/10643038
; Publication No. US2005014331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RFS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-038-20

Query Match      26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GCCTGGGATACCACTCTGG 31
Db 20 GCCTGGGATACCACTCTGG 1

RESULT 20
US-10-643-038-21/c
; Sequence 21, Application US/10643038
; Publication No. US2005014331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RFS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; CURRENT FILING DATE: 2003-08-18
```

Query Match 26.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-643-038-21

Query Match 26.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCTCTGAG 42  
DB 20 CAACTCTGGAGTCTCTGAG 1

RESULT 21  
US-10-643-038-22/c  
Sequence 22, Application US/10643038  
Publication No. US20050143331A1  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX  
FILE REFERENCE: RTS-0221  
CURRENT APPLICATION NUMBER: US/10/643,038  
CURRENT FILING DATE: 2003-08-18  
PRIOR APPLICATION NUMBER: US/09/865,866  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 173  
SEQ ID NO 22  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-643-038-22

Query Match 26.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTCTCTGAGAGGTAAGAG 52  
DB 20 GTCTCTGAGAGGTAAGAG 1

RESULT 22  
US-10-643-038-23/c  
Sequence 23, Application US/10643038  
Publication No. US20050143331A1  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX  
FILE REFERENCE: RTS-0221  
CURRENT APPLICATION NUMBER: US/10/643,038  
CURRENT FILING DATE: 2003-08-18  
PRIOR APPLICATION NUMBER: US/09/865,866  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 173  
SEQ ID NO 23  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-643-038-23

Query Match 26.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 CTCTGAGAGGTAAGAGCCA 55  
DB 20 CTCTGAGAGGTAAGAGCCA 1

RESULT 23  
US-10-643-038-24/c  
Sequence 24, Application US/10643038  
Publication No. US20050143331A1  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX  
FILE REFERENCE: RTS-0221  
CURRENT APPLICATION NUMBER: US/10/643,038  
CURRENT FILING DATE: 2003-08-18  
PRIOR APPLICATION NUMBER: US/09/865,866  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 173  
SEQ ID NO 24  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-643-038-24

Query Match 26.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGAGGTAAGAGCCGCGAA 60  
DB 20 AGAGGTAAGAGCCGCGAA 1

RESULT 24  
US-10-643-038-25/c  
Sequence 25, Application US/10643038  
Publication No. US20050143331A1  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX  
FILE REFERENCE: RTS-0221  
CURRENT APPLICATION NUMBER: US/10/643,038  
CURRENT FILING DATE: 2003-08-18  
PRIOR APPLICATION NUMBER: US/09/865,866  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 173  
SEQ ID NO 25  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-643-038-25

Query Match 26.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTGCAAG 77  
DB 20 GAAGCTGATGTCCTGCAAG 1

RESULT 25  
US-10-847-918-6072/c



```
; Sequence 6072, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6072
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai-antisense strand
; US-10-847-918-6072

Query Match      23.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 AAGAGCCAGCGAGCTGATGT 68
Db 21 AAAAGCCAGCGAGCTGATGT 1

RESULT 26
US-11-036-317-81949/c
; Sequence 81949, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-81949

Query Match      23.1%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 51 AGCCAGCGAGCTGATCTCT 71
Db 23 AGCCAGCGAGCTGATCTACT 3

RESULT 27
US-11-036-317-589182/c
; Sequence 589182, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
```

```
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 589182
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-589182

Query Match      23.1%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 20 ATACAACCTCTGGAGTCTCTG 40
Db 22 ATACAACGCTGGAGTCTCTATG 2

RESULT 28
US-10-719-956-632892/c
; Sequence 632892, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 632892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-632892

Query Match      22.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 47 AAAGAGCCGCGAGCTGATGTC 70
Db 25 AAAGAGCGAGCGAAGTTGTTGCC 2

RESULT 29
US-10-719-900-154278/c
; Sequence 154278, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 154278
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-154278

Query Match      22.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 46 TAAAGAGCGAGCGAAGCTGATGTC 69
```

```
Db      25 TAAAGAGCGACGGAAGCTCAGCTC 2
RESULT 30
US-10-719-900-338409
; Sequence 338409, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 338409
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-338409
Query Match      22.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      26 CTCTGGAGTCCTCTGAGAGGTAAA 49
      | | | | | | | | | | | | | | | |
Db      2 CACTGGAGGCTCTGACAGGGNAA 25

RESULT 31
US-10-422-475-4
; Sequence 4, Application US/10422475
; Publication No. US20030235813A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank
; APPLICANT: De Bari, Cosimo
; APPLICANT: Dell'Accio, Francesco
; TITLE OF INVENTION: In vivo assay and molecular markers for testing the phenotypic
; TITLE OF INVENTION: stability of cell populations and selecting cell populations for
; FILE REFERENCE: T2420-US
; CURRENT APPLICATION NUMBER: US/10/422,475
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 60/375,218
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: EP 99203273.0
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: RASP-A PLA2 sense primer
US-10-422-475-4
Query Match      22.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CAACTCTGGAGTCCTCT 39
      | | | | | | | | | | | | | | | |
Db      4 CAACTCTGGAGTCCTCT 20

RESULT 32
US-10-847-918-5566
; Sequence 5566, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5566
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-5566
Query Match      21.8%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      49 AGAGCCAGCGAAGCTGATGT 68
      | | | | | | | | | | | | | | | |
Db      1 AAAGCCAGCGACGCTGATGT 20

RESULT 33
US-10-847-918-5568/c
; Sequence 5568, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5568
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-847-918-5568
Query Match      21.8%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      49 AGAGCCAGCGAAGCTGATGT 68
      | | | | | | | | | | | | | | | |
Db      21 AAAGCCAGCGACGCTGATGT 2

RESULT 34
US-10-847-918-6070
; Sequence 6070, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
```

```

; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6070
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-6070

Query Match      21.8%; Score 16.4; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 49 AGACCCAGCGAGCTGATGT 68
| | | | | | | | | | | | | | | | | | | | |
Db 2 AAAGCCAGCGAGCTGATGT 21

RESULT 35
US-10-847-918-5567
; Sequence 5567, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5567
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai-sense strand
US-10-847-918-5567

Query Match      21.3%; Score 16.4; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAGCTGATGT 68
| | | | | | | | | | | | | | | | | | | | |
Db 1 AGCCAGCGAGCTGATGT 18

RESULT 36
US-10-847-918-5569
; Sequence 5569, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20

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; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5569
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-5569

Query Match      21.3%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAGCTGATGT 68
| | | | | | | | | | | | | | | | | | | | |
Db 2 AGCCAGCGAGCTGATGT 19

RESULT 37
US-10-847-918-5571/c
; Sequence 5571, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5571
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai-antisense strand
US-10-847-918-5571

Query Match      21.3%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAGCTGATGT 68
| | | | | | | | | | | | | | | | | | | | |
Db 20 AGCCAGCGAGCTGATGT 3

RESULT 38
US-10-847-918-6071
; Sequence 6071, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6071
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai-sense strand
US-10-847-918-6071

```

```
Query Match      21.3%; Score 16.4; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 51 AGCCAGCGAAGCTGATGT 68
      ||||| ||||| ||||| |||||
DB 2 AGCCAGCGACGUGAUGU 19

RESULT 39
US-10-847-918-5570
; Sequence 5570, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: G1896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; PRIOR FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5570
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai-sense strand
US-10-847-918-5570

Query Match      20.0%; Score 15.4; DB 1; Length 21;
Best Local Similarity 76.5%; Pred. No. 34;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 52 GCCAGCGAAGCTGATGT 68
      ||||| ||||| ||||| |||||
DB 1 GCCAGCGACGUGAUGU 17

RESULT 40
US-10-509-738-15
; Sequence 15, Application US/10509738
; Publication No. US2005020431A1
; GENERAL INFORMATION:
; APPLICANT: Director-General of National Institute of Advanced Industrial Science and Technology; Info Genes Co., Ltd.; Kazusa DNA Research Institute
; TITLE OF INVENTION: Application of KIAA0172 gene functions for therapeutics, diagnostics and pharmaceuticals
; FILE REFERENCE: PH-1610-PCT
; CURRENT APPLICATION NUMBER: US/10/509,738
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: JP 2002/99422
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-509-738-15

Query Match      20.0%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 60 AGCTGATGCTCTGTCAA 76
      ||||| ||||| ||||| |||||
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DB 2 AGCTGATGCTCTGTCAA 18

RESULT 41
US-10-751-736-9539/c
; Sequence 9539, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai
US-10-751-736-9539

Query Match      19.7%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 24 AACTCTGGAGTCTCTGAGA 43
      ||||| ||||| ||||| |||||
DB 21 AACTCAGGAGTCTCTGAGAGA 2

RESULT 42
US-10-751-736-16743/c
; Sequence 16743, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16743
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai
US-10-751-736-16743

Query Match      19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 39;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 31 GACTCCTCTGAGAGGTAA 48
      ||||| ||||| ||||| |||||
DB 18 GATTACTCTGAGAGGTAA 1

RESULT 43
US-10-751-736-17280/c
; Sequence 17280, Application US/10751736
; Publication No. US20040265230A1
```

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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751.736
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; NUMBER OF SEQ ID NOS: 06
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17280
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-17280

Query Match      19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 39;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 31 GAGTCCTCTGAGAGGTAA 48
Db 18 GATTACTCTGAGAGGTAA 1

RESULT 44
US-10-679-366-14/c
; Sequence 14, Application US/10679366
; Publication No. US20050059025A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Wei
; APPLICANT: Wu, Leeyang
; TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
; FILE REFERENCE: AM101072
; CURRENT APPLICATION NUMBER: US/10/679,366
; CURRENT FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-679-366-14

Query Match      19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 39;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 24 AACCTCGAGTCCTCTCA 41
Db 21 AAGCTAGAGTCCTCTCA 4

RESULT 45
US-10-847-918-5564
; Sequence 5564, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
```

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; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5564
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-5564

Query Match      19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 49 AGAGCCAGCGAGCTGAT 66
Db 3 AAAGCCAGCGAGCGCGAU 20

RESULT 46
US-09-866-108-10026
; Sequence 10026, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 10026
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10026

Query Match      18.7%; Score 14.4; DB 1; Length 17;
```

[illegible]

RESULT 47

US-09-866-108-10027  
US-09-866-108-10027, Application US/09866108  
US-09-866-108-10027, Application US/09866108  
Patent No. US20020048800A1  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharron G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: ABOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/006666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006657  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006655  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 60/266,860  
PRIOR FILING DATE: 2001-02-05  
NUMBER OF SEQ ID NOS: 15752  
SOFTWARE: Acomica Sequence Listing Engine  
SEQ ID NO 10027  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108-10027

RESULT 48  
US-10-723-361-10026

```

; Sequence 10026, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15/55
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10026
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-723-361-10026

Query Match      18.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      27  TCTGGAGTCCTCTGAG 42
Db      2  TCTGGAGTCCTCTGTG 17
          |||||
          |||||

RESULT 49
US-10-723-361-10027
; Sequence 10027, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6

```

RESULT 49  
US-10-723-361-10027  
; Sequence 10027, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POL  
; FILE REFERENCE: PB0105  
; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6

```
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 10027
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10027

Query Match      18.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      27 TCTGGAGTCTCTCTGAG 42
Db      1 TCTGGAGTCTCTCTG 16

RESULT 50
US-09-866-108-10024
; Sequence 10024, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00660
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 10025
; LENGTH: 17
```

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 10024
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10024

Query Match      18.2%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 TCTGGAGTCTCTCTG 40
Db      4 TCTGGAGTCTCTCTG 17

RESULT 51
US-09-866-108-10025
; Sequence 10025, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 10025
; LENGTH: 17
```

; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-10025

Query Match 18.2%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCG 40  
|||||

Db 3 TCTGGAGTCTCTCG 16

## RESULT 52

US-10-723-361-10024  
; Sequence 10024, Application US/10723361

; Publication No. US20040137589A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105

; CURRENT APPLICATION NUMBER: US/10/723,361

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 10024

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-723-361-10024

## Query Match

Best Local Similarity 18.2%; Score 14; DB 1; Length 17;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCG 40  
|||||

Db 4 TCTGGAGTCTCTCG 17

## RESULT 53

US-10-723-361-10025

; Sequence 10025, Application US/10723361

; Publication No. US20040137589A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105

; CURRENT APPLICATION NUMBER: US/10/723,361

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 10025

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-723-361-10025

## Query Match

Best Local Similarity 18.2%; Score 14; DB 1; Length 17;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCG 40  
|||||

Db 3 TCTGGAGTCTCTCG 16

## RESULT 54

US-10-060-998-930/c

; Sequence 930, Application US/10060998

; Publication No. US20030104530A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1

; FILE REFERENCE: PB01108

; CURRENT APPLICATION NUMBER: US/10/060,998

; CURRENT FILING DATE: 2002-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 09/864,761

; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/343,331

; PRIOR FILING DATE: 2001-12-21

; NUMBER OF SEQ ID NOS: 3056

; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 930

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-060-998-930

## Query Match

Best Local Similarity 17.9%; Score 13.8; DB 1; Length 17;



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Best Local Similarity 88.2%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGCGAGCT 63
Db 17 AATGAGCCAGCGAAGAT 1

RESULT 55
US-09-866-108-10028
; Sequence 10028, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wenaheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 10028
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10028

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGGAGTCCTCTGAG 42
Db 1 CTGGAGTCCTCTGAG 15

RESULT 56
US-10-060-998-931/c
; Sequence 931, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 931
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-932

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGCGAAG 61
Db 15 AATGAGCCAGCGAAG 1

RESULT 58
US-10-723-361-10028
; Sequence 10028, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
```

```
; Sequence 931, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 931
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-931

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGCGAAG 61
Db 16 AATGAGCCAGCGAAG 2

RESULT 57
US-10-060-998-932/c
; Sequence 932, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 932
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-932

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGCGAAG 61
Db 15 AATGAGCCAGCGAAG 1

RESULT 58
US-10-723-361-10028
; Sequence 10028, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
```



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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10023
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10023

Query Match      16.9%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      27 TCTGGAGTCTCTCT 39
Db      5 TCTGGAGTCTCTCT 17

RESULT 62
US-10-723-361-10023
; Sequence 10023, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; CURRENT APPLICATION NUMBER: US/10/723,361
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
```

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10023
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10023

Query Match      16.9%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      27 TCTGGAGTCTCTCT 39
Db      5 TCTGGAGTCTCTCT 17

RESULT 63
US-10-367-980A-11/c
; Sequence 11, Application US/10367980A
; Publication No. US20030228592A1
; GENERAL INFORMATION:
; APPLICANT: St Vincent's Institute of Medical Research
; APPLICANT: Rogers, Suzanne D
; APPLICANT: Best, James D
; TITLE OF INVENTION: Human Facilitative Glucose Transport Protein GLUT8
; FILE REFERENCE: VS:AJH:FP17928
; CURRENT APPLICATION NUMBER: US/10/367,980A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 09/509,731
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: PCR primer (reverse)
US-10-367-980A-11

Query Match      16.9%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      50 GAGCCGACGGAAGC 62
Db      14 GAGCCGACGGAAGC 2

RESULT 64
US-10-060-998-929/c
; Sequence 929, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
```

```
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 929
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-929

Query Match      16.6%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;

QY 48 AAGAGCCGCGAAGCT 63
Db 17 ATGAGCCGCGAAGAT 2

RESULT 65
US-10-469-277-7
; Sequence 7, Application US/10469277
; Publication No. US20040170996A1
; GENERAL INFORMATION:
; APPLICANT: Yee, Leland
; APPLICANT: Tang, Jianming
; APPLICANT: Kaslow, Richard A.
; APPLICANT: van Leeuwen, Dirk J.
; TITLE OF INVENTION: CYTOTOXIC T-LYMPHOCYTE ANTIGEN-4 OR INTERLEUKIN-10 POLYMORPHISMS
; TITLE OF INVENTION: AS PREDICTORS OF RESPONSE TO THERAPEUTIC INTERVENTION
; FILE REFERENCE: UAB-19302/22
; CURRENT APPLICATION NUMBER: US/10/469,277
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/US02/06207
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/271,811
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Reverse primer
US-10-469-277-7

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;

QY 47 AAAGAGCCGCGAAGC 62
Db 1 ACAGAGCCGCGCAAGC 16

RESULT 66
US-09-866-108-10029
; Sequence 10029, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
```

```
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10029
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10029

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTGAG 42
Db 1 TGGAGTCCTCTGTG 14

RESULT 67
US-09-825-805-816
; Sequence 816, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MEH800-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
```

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; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 816
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-816

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 28 CTGAGTCCTCTGA 41
Db 4 CUGAGCCCUUGA 17

RESULT 68
US-10-060-998-927/c
; Sequence 927, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 927
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-927

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAAGCT 63
Db 17 GAGCCAGCGAAGAT 4

RESULT 69
US-10-060-998-928/c
; Sequence 928, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 928
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-928
```

```
; SEQ ID NO 928
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-928

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAAGCT 63
Db 16 GAGCCAGCGAAGAT 3

RESULT 70
US-10-060-998-933/c
; Sequence 933, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 933
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-933

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAA 60
Db 14 AATGAGCCAGCGAA 1

RESULT 71
US-10-163-552-786
; Sequence 786, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; TITLE OF INVENTION: HER2
; FILE REFERENCE: MBH01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 786
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-786

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 28 CTGAGTCCTCTGA 41
```

Db 4 CUGGAGCCUCUGA 17  
|:||||| |:|:|

## RESULT 72

US-10-138-674-7914  
; Sequence 7914, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7914  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674-7914

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 64.3%; Pred. No. 52;  
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 26 CTCTGGAGTCCTCT 39  
|:||||| |:|:|

Db 2 CUGGGAGGUCUCU 15

## RESULT 73

US-10-287-949A-7914  
; Sequence 7914, Application US/10287949A  
; Publication No. US20040102389A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7914  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949A-7914

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 64.3%; Pred. No. 52;  
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 26 CTCTGGAGTCCTCT 39  
|:||||| |:|:|

Db 2 CUGGGAGGUCUCU 15

## RESULT 74

US-10-723-361-10029  
; Sequence 10029, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI  
; FILE REFERENCE: PB0105  
; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 10029  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-361-10029

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 52;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 29 TGGAGTCCTCTGAG 42

Db 1 TGGAGTCCTCTGAG 14

## RESULT 75

US-10-712-633-1056  
; Sequence 1056, Application US/10712633  
; Publication No. US20040220128A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Sandberg, Jennifer  
; APPLICANT: Gordon, Gilad  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTO  
; FILE REFERENCE: MBH02-325PCT (400/047)  
; CURRENT APPLICATION NUMBER: US/10/712,633  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 09/708,690  
; PRIOR FILING DATE: 2000-11-07

; PRIOR APPLICATION NUMBER: US 09/870,161  
 ; PRIOR FILING DATE: 2001-05-29  
 ; PRIOR APPLICATION NUMBER: US 60/334,461  
 ; PRIOR FILING DATE: 2001-11-30  
 ; PRIOR APPLICATION NUMBER: US 10/138,674  
 ; PRIOR FILING DATE: 2002-05-03  
 ; NUMBER OF SEQ ID NOS: 5989  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1056  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo Sapiens  
 US-10-712-633-1056

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 64.3%; Pred. No. 52;  
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 26 CTCCTGGAGTCTCT 39  
 |||||:|:|:  
 Db 2 CUCGGAGUCCUCU 15

## RESULT 76

US-10-724-270-5441  
 ; Sequence 5441, Application US/10724270  
 ; Publication No. US20050080031A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sirna Therapeutics, Inc.  
 ; APPLICANT: McSwiggen, James  
 ; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level  
 ; TITLE OF INVENTION: RAS, HER2 and HIV  
 ; FILE REFERENCE: 400/046-US (MEHB02-326-A)  
 ; CURRENT APPLICATION NUMBER: US/10/724,270  
 ; CURRENT FILING DATE: 2003-11-26  
 ; PRIOR APPLICATION NUMBER: PCT/US02/16840  
 ; PRIOR FILING DATE: 2002-05-29  
 ; PRIOR APPLICATION NUMBER: US 60/318,471  
 ; PRIOR FILING DATE: 2001-09-10  
 ; PRIOR APPLICATION NUMBER: US 60/296,249  
 ; PRIOR FILING DATE: 2001-06-06  
 ; PRIOR APPLICATION NUMBER: US 60/294,140  
 ; PRIOR FILING DATE: 2001-05-29  
 ; PRIOR APPLICATION NUMBER: US 10/238,700  
 ; PRIOR FILING DATE: 2002-09-10  
 ; PRIOR APPLICATION NUMBER: US 10/163,552  
 ; PRIOR FILING DATE: 2002-06-06  
 ; PRIOR APPLICATION NUMBER: US 10/157,580  
 ; PRIOR FILING DATE: 2002-05-29  
 ; PRIOR APPLICATION NUMBER: US 10/693,059  
 ; PRIOR FILING DATE: 2002-10-23  
 ; PRIOR APPLICATION NUMBER: US 10/444,853  
 ; PRIOR FILING DATE: 2003-05-23  
 ; PRIOR APPLICATION NUMBER: US 10/417,012  
 ; PRIOR FILING DATE: 2003-04-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 6810  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5441  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-10-724-270-5441

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 71.4%; Pred. No. 52;  
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTCGAGTCTCTGA 41  
 |||||:|:|:  
 Db 4 CUGGAGCCUCUGA 17

RESULT 77  
 US-09-864-785-2825/c  
 ; Sequence 2825, Application US/09864785  
 ; Patent No. US20020177568A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Stinchcomb, Dan  
 ; APPLICANT: Draper, Ken  
 ; APPLICANT: McSwiggen, Jim  
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
 ; TITLE OF INVENTION: Levels of NP-Kappa B  
 ; FILE REFERENCE: 400/022 (MEHB00-812-D)  
 ; CURRENT APPLICATION NUMBER: US/09/864,785  
 ; CURRENT FILING DATE: 2001-05-23  
 ; NUMBER OF SEQ ID NOS: 3929  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 2825  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
 US-09-864-785-2825

Query Match 15.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 55;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AAGAGCGCTGGGATA 22  
 |||||:|:|:  
 Db 17 AGGAGCGCTGGGCTA 1

## RESULT 78

US-09-930-423-1056  
 ; Sequence 1056, Application US/09930423  
 ; Publication No. US2003002003A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Blatt, Larry  
 ; APPLICANT: McSwiggen, Jim  
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
 ; FILE REFERENCE: MEHB00,918-A 400/027  
 ; CURRENT APPLICATION NUMBER: US/09/930,423  
 ; CURRENT FILING DATE: 2001-08-15  
 ; NUMBER OF SEQ ID NOS: 4553  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1056  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo Sapiens  
 US-09-930-423-1056

Query Match 15.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 58.8%; Pred. No. 55;  
 Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 61 GCTGATGCTCTGCAAG 77  
 ||:|:|:|:|:  
 Db 1 GCUGGUGUGCGGCAAG 17

## RESULT 79

US-09-745-237A-1056  
 ; Sequence 1056, Application US/09745237A  
 ; Publication No. US20030143708A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Blatt, Larry  
 ; APPLICANT: McSwiggen, Jim  
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
 ; FILE REFERENCE: 400/007 (MEHB00-918-A)  
 ; CURRENT APPLICATION NUMBER: US/09/745,237A





```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Primer
US-10-913-280-108

Query Match      15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 53;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 25 ACTCTGGAGTCCTCTGA 41
Db 1 ACACAGCGCTCCTCTGA 17

RESULT 84
US-10-776-934-113
; Sequence 113, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THURUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 113
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-776-934-113

Query Match      15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64
Db 4 CCAGCGAAGCTG 15

RESULT 85
US-10-776-934-592
; Sequence 592, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THURUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
```

```
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 592
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-776-934-592

Query Match      15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64
Db 4 CCAGCGAAGCTG 15

RESULT 86
US-10-776-934-593
; Sequence 593, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THURUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 593
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-776-934-593

Query Match      15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64
Db 4 CCAGCGAAGCTG 15

RESULT 87
US-10-776-934-594
; Sequence 594, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THURUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 594
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-776-934-594

Query Match      15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64
Db 4 CCAGCGAAGCTG 15

RESULT 88
US-10-776-934-595
; Sequence 595, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THURUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
```

```
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64
    |||||
Db 4 CCAGCGAAGCTG 15

RESULT 87
US-10-776-934-594
; Sequence 594, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRU, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR FILING DATE: 2003-02-10
; PRIOR FILING DATE: 2003-02-10
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 594
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: modified base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (13)..(16)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)..(13)
; OTHER INFORMATION: phosphorothioate linkage
US-10-776-934-594

Query Match 15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64
    |||||
Db 4 CCAGCGAAGCTG 15

RESULT 88
US-10-776-934-595
; Sequence 595, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRU, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR FILING DATE: 2003-02-10
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
```

```
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 595
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorothioate linkage
US-10-776-934-595

Query Match 15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64
    |||||
Db 4 CCAGCGAAGCTG 15

RESULT 89
US-09-866-108-10022
; Sequence 10022, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 10022
```

; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-10022

Query Match 15.6%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTC 38  
|||||  
DB 6 TCTGGAGTCTCTC 17

## RESULT 90

US-10-723-361-10022  
; Sequence 10022, Application US/10723361  
; Publication No. US20040137589A1

## GENERAL INFORMATION:

; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105

; CURRENT APPLICATION NUMBER: US/10/723,361

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeonica Sequence Listing Engine

; SEQ ID NO 10022

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-723-361-10022

Query Match 15.6%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTC 38  
|||||  
DB 6 TCTGGAGTCTCTC 17

## RESULT 91

US-10-138-674-6986/c

; Sequence 6986, Application US/10138674

; Publication No. US20040077565A1

## GENERAL INFORMATION:

; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MEHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6986  
; LENGTH: 16  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674-6986

Query Match 15.3%; Score 11.8; DB 1; Length 16;  
Best Local Similarity 86.7%; Pred. No. 55;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 52 GCCAGCGAAGCTGAT 66  
|||||  
DB 16 GCCAGCATAGCTGAT 2

## RESULT 92

US-10-287-949A-6986/c

; Sequence 6986, Application US/10287949A

; Publication No. US20040102389A1

## GENERAL INFORMATION:

; APPLICANT: Ribozyne Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; FILE REFERENCE: MEHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/287,949A

; CURRENT FILING DATE: 2003-04-11

; NUMBER OF SEQ ID NOS: 20822

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6986

; LENGTH: 16

; TYPE: RNA

; ORGANISM: Homo sapiens

US-10-287-949A-6986

Query Match 15.3%; Score 11.8; DB 1; Length 16;  
Best Local Similarity 86.7%; Pred. No. 55;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 52 GCCAGCGAAGCTGAT 66  
|||||  
DB 16 GCCAGCATAGCTGAT 2

## RESULT 93

US-10-741-600-73537/c

; Sequence 73537, Application US/10741600

; Publication No. US20050026169A1

## GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 73537

```
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-73537

Query Match      15.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 31 GAGTCCTCTGAGAGG 45
Db 16 GAGTCCTCCGGAGG 2

RESULT 94
US-10-257-017B-41787
; Sequence 41787, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 41787
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012525
US-10-257-017B-41787

Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAGA 51
Db 1 TGAGAGGTAAGA 13

RESULT 95
US-10-257-017B-41788/c
; Sequence 41788, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 41788
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012525
US-10-257-017B-41788

Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAGA 51
Db 13 TGAGAGGTAAGA 1

RESULT 96
US-10-257-017B-184441
; Sequence 184441, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 184441
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045516
US-10-257-017B-184441

Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAGA 51
Db 1 TGAGATGTAAGA 13

RESULT 97
US-10-257-017B-184442/c
; Sequence 184442, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 184442
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045516
US-10-257-017B-184442

Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAGA 51
Db 13 TGAGATGTAAGA 1
```

```

RESULT 98
US-10-142-729-26/c
; Sequence 26, Application US/10142729
; Publication No. US20030165888A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; FILE REFERENCE: OASBIO.005A
; CURRENT APPLICATION NUMBER: US/10/142,729
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-142-729-26

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GATCAACTCTGGAG 33
Db 15 GATACNGCTCTNGAG 1

RESULT 99
US-10-142-729-39/c
; Sequence 39, Application US/10142729
; Publication No. US20030165888A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; FILE REFERENCE: OASBIO.005A
; CURRENT APPLICATION NUMBER: US/10/142,729
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-142-729-39

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GATCAACTCTGGAG 33
Db 15 GATACNGCTCTNGAG 1

RESULT 100
US-10-375-504-26/c
; Sequence 26, Application US/10375504
; Publication No. US20030170711A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; FILE REFERENCE: OASBIO.005C1
; CURRENT APPLICATION NUMBER: US/10/375,504
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 10/142,729
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-375-504-26

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GATCAACTCTGGAG 33
Db 15 GATACNGCTCTNGAG 1

RESULT 101
US-10-375-504-39/c
; Sequence 39, Application US/10375504
; Publication No. US20030170711A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; FILE REFERENCE: OASBIO.005C1
; CURRENT APPLICATION NUMBER: US/10/375,504
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 10/142,729
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94

```

```

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GATCAACTCTGGAG 33
Db 15 GATACNGCTCTNGAG 1

RESULT 100
US-10-375-504-26/c
; Sequence 26, Application US/10375504
; Publication No. US20030170711A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; FILE REFERENCE: OASBIO.005C1
; CURRENT APPLICATION NUMBER: US/10/375,504
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 10/142,729
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-375-504-26

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GATCAACTCTGGAG 33
Db 15 GATACNGCTCTNGAG 1

RESULT 101
US-10-375-504-39/c
; Sequence 39, Application US/10375504
; Publication No. US20030170711A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; FILE REFERENCE: OASBIO.005C1
; CURRENT APPLICATION NUMBER: US/10/375,504
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 10/142,729
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94

```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-375-504-39

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 19 GATCAACTCTGCAG 33
Db 15 GATACNGCTCTNGAG 1

RESULT 102
US-10-719-993-55182
; Sequence 55182, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55182
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-55182

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 CCTGGGGGATACAA 25
Db 1 CCGGGGGGATACAA 13

RESULT 103
US-09-875-453-65/c
; Sequence 65, Application US/09875453
; Publication No. US20030027320A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungseuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruce, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 4600-0135-30
; CURRENT APPLICATION NUMBER: US/09/875,453
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06

; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453-65

Query Match      14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 65;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 38 CTGAGAGGTAAAGAGC 53
Db 16 CTGGGAGGTGGAGAGC 1

RESULT 104
US-10-331-907-450
; Sequence 450, Application US/10331907
; Publication No. US20030181660A1
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. US20030181660A1el LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/10/331,907
; FILING DATE: 31-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J. Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 450:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 450:
US-10-331-907-450
```

Query Match 14.5%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 65;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 39 TGAGAGGTTAAAGAGCC 54  
Db 1 TCACAGGTAGGAGCC 16

## RESULT 105

US-10-407-807-67/c  
; Sequence 67, Application US/10407807  
; Publication No. US20040096848A1  
; GENERAL INFORMATION:  
; APPLICANT: THRUE, ANJA MOLHART  
; APPLICANT: HOG, ANJA MOLHART  
; APPLICANT: KRISTJANSEN, PAUL E.G.  
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION HIP-1ALPHA

; FILE REFERENCE: 57390 (45120)  
; CURRENT APPLICATION NUMBER: US/10/407,807  
; CURRENT FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: 60/370,126  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 67  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide  
US-10-407-807-67

Query Match 14.5%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 65;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGCGAAGC 62  
Db 16 AAACACACAGCGAAGC 1

## RESULT 106

US-10-450-797-548/c  
; Sequence 548, Application US/10450797  
; Publication No. US20040142335A1  
; GENERAL INFORMATION:  
; APPLICANT: Petersohn, Dirk  
; APPLICANT: Conradt, Marcus  
; APPLICANT: Hofmann, Kay  
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

; FILE REFERENCE: HENK-0041  
; CURRENT APPLICATION NUMBER: US/10/450,797  
; CURRENT FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: PCT/EP01/15178  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: DE 101 00 121.5  
; PRIOR FILING DATE: 2001-01-03  
; NUMBER OF SEQ ID NOS: 1435  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 548  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-450-797-548

Query Match 14.3%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATACAACCTCG 30  
Db 11 ATACAACCTCG 1

## RESULT 107

US-10-257-017B-320928/c  
; Sequence 320928, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:

; APPLICANT: Alexander Olek  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 320928  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029975

US-10-257-017B-320928

Query Match 14.3%; Score 11; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GAGAGGTAAAG 50  
Db 12 GAGAGGTAAAG 2

## RESULT 108

US-10-257-017B-14593  
; Sequence 14593, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:

; APPLICANT: Alexander Olek  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 14593  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003290

US-10-257-017B-14593

Query Match 14.3%; Score 11; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 48;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 41 AGAGGTAAAGAC 53  
Db 1 AGAAGTAAAGAGY 13

## RESULT 109

US-10-257-017B-14594/c

```

; Sequence 14594, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 14594
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003290
US-10-257-017B-14594

Query Match      14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGAGGTAAGAGC 53
Db 13 AGAAGTAAGAGY 1

RESULT 110
US-10-257-017B-181997
; Sequence 181997, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 181997
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044987
US-10-257-017B-181997

Query Match      14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAAG 49
Db 2 TGAGAGGTAAAG 12

RESULT 111
US-10-257-017B-181998/c
; Sequence 181998, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

```

```

; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 181998
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044987
US-10-257-017B-181998

Query Match      14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAAG 49
Db 12 TGAGAGGTAAAG 2

RESULT 112
US-10-257-017B-224917
; Sequence 224917, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 224917
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054826
US-10-257-017B-224917

Query Match      14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGAGGTAAGAGA 51
Db 2 AGAGGTAAGAGA 12

RESULT 113
US-10-257-017B-224918/c
; Sequence 224918, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046

```



```
; SEQ ID NO 224918
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054826
US-10-257-017B-224918

Query Match      14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      41 AGAGGTAAGA 51
DB      12 AGAGGTAAGA 2
        |||||
        |||||

RESULT 114
US-09-998-027-20
; Sequence 20, Application US/09998027
; Publication No. US20030093819A1
; GENERAL INFORMATION:
; APPLICANT: D'Andrea et al.
; TITLE OF INVENTION: Methods and Compositions for the
; TITLE OF INVENTION: Diagnosis and Treatment of Cancers Associated with Defective
; TITLE OF INVENTION: DNA Repair Mechanisms
; FILE REFERENCE: 2486/101
; CURRENT APPLICATION NUMBER: US/09/998,027
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; OTHER INFORMATION: Intron/Exon Junctions of PANCD
US-09-998-027-20

Query Match      14.3%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      43 AGCTAAAGAGC 53
DB      2 AGCTAAAGAGC 12
        |||||
        |||||

RESULT 115
US-10-165-099-20
; Sequence 20, Application US/10165099
; Publication No. US20030188326A1
; GENERAL INFORMATION:
; APPLICANT: D'Andrea, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS OF CANCER SUSCEPTIBILITY
; TITLE OF INVENTION: DEFECTIVE DNA REPAIR MECHANISMS AND TREATMENT THEREOF
; FILE REFERENCE: 7032/2055
; CURRENT APPLICATION NUMBER: US/10/165,099
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 09/998,027
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 60/245,756
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-165-099-20

Query Match      14.3%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 55;
```

```
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      43 AGCTAAAGAGC 53
DB      2 AGCTAAAGAGC 12
        |||||
        |||||

RESULT 116
US-09-504-231A-1178/c
; Sequence 1178, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: TPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1178
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1178

Query Match      14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GTAAAGAGCCA 55
DB      13 GTAAAGAGCCA 3
        |||||
        |||||

RESULT 117
US-09-504-231A-1179/c
; Sequence 1179, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: TPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
```

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1179
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1179

Query Match          14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GTAAAGAGCCA 55
Db      11 GTAAAGAGCCA 1

RESULT 118
US-09-274-553D-1178/c
; Sequence 1178, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: TPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1178
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1178

Query Match          14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GTAAAGAGCCA 55
Db      13 GTAAAGAGCCA 3

RESULT 119
US-09-274-553D-1179/c
; Sequence 1179, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: TPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
```

```
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1179
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1179

Query Match          14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GTAAAGAGCCA 55
Db      11 GTAAAGAGCCA 1

Search completed: April 19, 2006, 16:13:31
Job time : 0.001 secs
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 16:15:43 ; Search time 0.001 Seconds

(without alignments)

1028.104 Million cell updates/sec

Title: US-10-643-038-17\_994-1070

Perfect score: 77

Sequence: 1 caaacagacgcctgggga.....gaagctgagtctctgtcaag 77

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 351 seqs, 6676 residues

Total number of hits satisfying chosen parameters: 702

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 351 summaries

Database : pubnewdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

*Publi-shed - Applications - NA - New*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18.2	23.6	25	1	US-11-121-849-226711
C 2	17.6	22.9	25	1	US-11-121-849-18534
C 3	17.4	22.6	19	1	US-11-101-244-512380
C 4	17.4	22.6	19	1	US-11-083-784-512380
C 5	16.4	21.3	19	1	US-11-101-244-1197318
C 6	16.4	21.3	19	1	US-11-101-244-1197383
C 7	16.4	21.3	19	1	US-11-083-784-1197318
C 8	16.4	21.3	19	1	US-11-083-784-1197383
C 9	16.4	21.3	22	1	US-10-310-914A-1373610
C 10	16.2	21.0	21	1	US-10-310-914A-99908
C 11	16.2	21.0	23	1	US-10-310-914A-591217
C 12	16.2	21.0	23	1	US-10-310-914A-921349
C 13	15.8	20.5	21	1	US-10-972-767-181
C 14	15.8	20.5	22	1	US-11-069-908-3819
C 15	15.6	20.3	22	1	US-10-310-914A-1094322
C 16	15.4	20.0	19	1	US-11-101-244-826612
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C 18	15.4	20.0	19	1	US-11-101-244-1197395
C 19	15.4	20.0	19	1	US-11-101-244-1375618
C 20	15.4	20.0	19	1	US-11-083-784-826612
C 21	15.4	20.0	19	1	US-11-083-784-1197334
C 22	15.4	20.0	19	1	US-11-083-784-1197395
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C 27	15.2	19.7	21	1	US-10-310-914A-1213419
C 28	14.8	19.2	18	1	US-10-310-914A-45021
C 29	14.8	19.2	18	1	US-10-310-914A-921346
C 30	14.8	19.2	18	1	US-10-310-914A-946718
C 31	14.8	19.2	19	1	US-10-310-914A-1358783
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1	US-11-101-244-686504	19.2	14.8	35
1	US-11-101-244-716743	19.2	14.8	36
1	US-11-101-244-741998	19.2	14.8	37
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1	US-11-101-244-1221940	19.2	14.8	39
1	US-11-101-244-1222038	19.2	14.8	40
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1	US-11-083-784-462186	19.2	14.8	42
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1	US-11-101-244-1155118	18.7	14.4	55
1	US-11-101-244-1256070	18.7	14.4	56
1	US-11-101-244-1323244	18.7	14.4	57
1	US-11-101-244-1435551	18.7	14.4	58
1	US-11-101-244-1536025	18.7	14.4	59
1	US-11-101-244-1526053	18.7	14.4	60
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1	US-10-750-623-15591	18.7	14.4	71
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1	US-11-101-244-716725	18.4	14.2	80
1	US-11-101-244-749629	18.4	14.2	81
1	US-11-101-244-819751	18.4	14.2	82
1	US-11-101-244-840452	18.4	14.2	83
1	US-11-101-244-931449	18.4	14.2	84
1	US-11-101-244-1006983	18.4	14.2	85
1	US-11-101-244-1178034	18.4	14.2	86
1	US-11-101-244-1238798	18.4	14.2	87
1	US-11-101-244-1257649	18.4	14.2	88
1	US-11-101-244-1286557	18.4	14.2	89
1	US-11-101-244-1327450	18.4	14.2	90
1	US-11-101-244-1402806	18.4	14.2	91
1	US-11-101-244-1508424	18.4	14.2	92
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1	US-11-083-784-518286	18.4	14.2	95
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1	US-11-083-784-539604	18.4	14.2	97
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1	US-11-083-784-716725	18.4	14.2	99
1	US-11-083-784-749629	18.4	14.2	100
1	US-11-083-784-819751	18.4	14.2	101
1	US-11-083-784-840452	18.4	14.2	102
1	US-11-083-784-931449	18.4	14.2	103
1	US-11-083-784-1006983	18.4	14.2	104
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1	US-11-083-784-1238798	18.4	14.2	106

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c 129	13.8	17.9	19	1	US-10-310-914A-1194348	Sequence 1194348,	c 202	13.8	17.9	19	1	US-11-083-784-1286508	Sequence 1286508,
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c 281 13.4 17.4 19 1 US-11-083-784-276236 Sequence 276236,
c 282 13.4 17.4 19 1 US-11-083-784-387184 Sequence 387184,
c 283 13.4 17.4 19 1 US-11-083-784-387289 Sequence 387289,
c 284 13.4 17.4 19 1 US-11-083-784-387392 Sequence 387392,
c 285 13.4 17.4 19 1 US-11-083-784-387492 Sequence 387492,
c 286 13.4 17.4 19 1 US-11-083-784-410730 Sequence 410730,
c 287 13.4 17.4 19 1 US-11-083-784-410929 Sequence 410929,
c 288 13.4 17.4 19 1 US-11-083-784-411027 Sequence 411027,
c 289 13.4 17.4 19 1 US-11-083-784-512370 Sequence 512370,
c 290 13.4 17.4 19 1 US-11-083-784-527876 Sequence 527876,
c 291 13.4 17.4 19 1 US-11-083-784-539325 Sequence 539325,
c 292 13.4 17.4 19 1 US-11-083-784-550822 Sequence 550822,
c 293 13.4 17.4 19 1 US-11-083-784-550923 Sequence 550923,
c 294 13.4 17.4 19 1 US-11-083-784-581627 Sequence 581627,
c 295 13.4 17.4 19 1 US-11-083-784-624448 Sequence 624448,
c 296 13.4 17.4 19 1 US-11-083-784-680973 Sequence 680973,
c 297 13.4 17.4 19 1 US-11-083-784-686033 Sequence 686033,
c 298 13.4 17.4 19 1 US-11-083-784-710507 Sequence 710507,
c 299 13.4 17.4 19 1 US-11-083-784-710553 Sequence 710553,
c 300 13.4 17.4 19 1 US-11-083-784-785114 Sequence 785114,
c 301 13.4 17.4 19 1 US-11-083-784-785140 Sequence 785140,
c 302 13.4 17.4 19 1 US-11-083-784-795267 Sequence 795267,
c 303 13.4 17.4 19 1 US-11-083-784-833429 Sequence 833429,
c 304 13.4 17.4 19 1 US-11-083-784-878459 Sequence 878459,
c 305 13.4 17.4 19 1 US-11-083-784-972375 Sequence 972375,
c 306 13.4 17.4 19 1 US-11-083-784-972474 Sequence 972474,
c 307 13.4 17.4 19 1 US-11-083-784-1012488 Sequence 1012488,
c 308 13.4 17.4 19 1 US-11-083-784-1034219 Sequence 1034219,
c 309 13.4 17.4 19 1 US-11-083-784-1036393 Sequence 1036393,
c 310 13.4 17.4 19 1 US-11-083-784-1155168 Sequence 1155168,
c 311 13.4 17.4 19 1 US-11-083-784-1235172 Sequence 1235172,
c 312 13.4 17.4 19 1 US-11-083-784-1249609 Sequence 1249609,
c 313 13.4 17.4 19 1 US-11-083-784-1326829 Sequence 1326829,
c 314 13.4 17.4 19 1 US-11-083-784-1327400 Sequence 1327400,
c 315 13.4 17.4 19 1 US-11-083-784-1327433 Sequence 1327433,
c 316 13.4 17.4 19 1 US-11-083-784-1351972 Sequence 1351972,
c 317 13.4 17.4 19 1 US-11-083-784-1359582 Sequence 1359582,
c 318 13.4 17.4 19 1 US-11-083-784-1359676 Sequence 1359676,
c 319 13.4 17.4 19 1 US-11-083-784-1418701 Sequence 1418701,
c 320 13.4 17.4 19 1 US-11-083-784-1435574 Sequence 1435574,
c 321 13.4 17.4 19 1 US-11-083-784-1492356 Sequence 1492356,
c 322 13.4 17.4 19 1 US-11-083-784-1512594 Sequence 1512594,
c 323 13.4 17.4 19 1 US-11-083-784-1522587 Sequence 1522587,
c 324 13.4 17.4 19 1 US-11-083-784-1560555 Sequence 1560555,
c 325 13.4 17.4 19 1 US-11-083-784-1570062 Sequence 1570062,

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326 13.4 17.4 19 1 US-11-083-784-1570074 Sequence 1570074,
327 13.4 17.4 19 1 US-11-083-784-1590808 Sequence 1590808,
c 328 13.2 17.1 18 1 US-10-310-914A-128513 Sequence 128513,
329 13.2 17.1 18 1 US-10-310-914A-176877 Sequence 176877,
330 13.2 17.1 18 1 US-10-310-914A-721777 Sequence 721777,
331 13.2 17.1 18 1 US-10-310-914A-794232 Sequence 794232,
332 13.2 17.1 18 1 US-10-310-914A-956449 Sequence 956449,
c 333 13.2 17.1 18 1 US-10-310-914A-970022 Sequence 970022,
c 334 13.2 17.1 18 1 US-10-310-914A-1268240 Sequence 1268240,
335 13 16.9 18 1 US-10-310-914A-1213531 Sequence 1213531,
c 336 12.8 16.6 18 1 US-10-750-185-15896 Sequence 15896, A
c 337 12.8 16.6 18 1 US-10-750-623-15896 Sequence 15896, A
338 12.8 16.6 18 1 US-10-310-914A-198185 Sequence 198185,
339 12.8 16.6 18 1 US-10-310-914A-319191 Sequence 319191,
c 340 12.8 16.6 18 1 US-10-310-914A-537246 Sequence 537246,
c 341 12.8 16.6 18 1 US-10-310-914A-560230 Sequence 560230,
c 342 12.8 16.6 18 1 US-10-310-914A-575025 Sequence 575025,
c 343 12.8 16.6 18 1 US-10-310-914A-586396 Sequence 586396,
c 344 12.8 16.6 18 1 US-10-310-914A-784421 Sequence 784421,
345 12.8 16.6 18 1 US-10-310-914A-815477 Sequence 815477,
c 346 12.8 16.6 18 1 US-10-310-914A-919520 Sequence 919520,
c 347 12.8 16.6 18 1 US-10-310-914A-1087593 Sequence 1087593,
c 348 12.8 16.6 18 1 US-10-310-914A-1209729 Sequence 1209729,
c 349 12.8 16.6 18 1 US-10-310-914A-1353151 Sequence 1353151,
c 350 12.8 16.6 18 1 US-10-310-914A-1354913 Sequence 1354913,
c 351 12 15.6 12 1 US-10-505-263-37 Sequence 37, Appl

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## ALIGNMENTS

## RESULT 1

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US-11-121-849-226711/c
; Sequence 226711, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 226711
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-11-121-849-226711

```

```

Query Match 23.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

Qy 27 TCTGGAGTCTCTGAGAGGTAAA 49
|||

```

```

Db 24 TCAGGAGTCTCTTGGAGGTAAA 2
|||

```

## RESULT 2

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US-11-121-849-18534/c
; Sequence 18534, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949

```

```
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18534
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-18534
```

```
Query Match      22.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
QY 29 TGGAGTCTCTGAGAGGTAAGAG 52
Db 24 TGGAGTAACTGAGGGTAAGAG 1
```

## RESULT 3

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US-11-101-244-512380/c
; Sequence 512380, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 512380
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-512380
```

```
Query Match      22.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 23 CAACTCTGGAGTCTCTCTGA 41
Db 19 CAACACTGGAGTCTCTCTGA 1
```

## RESULT 4

```
US-11-083-784-512380/c
; Sequence 512380, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
```

```
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 512380
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-512380
```

```
Query Match      22.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 23 CAACTCTGGAGTCTCTCTGA 41
Db 19 CAACACTGGAGTCTCTCTGA 1
```

## RESULT 5

```
US-11-101-244-1197318
; Sequence 1197318, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1197318
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1197318
```

```
Query Match      21.3%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 58 GAAGCTGATGTCCTCTGCA 75
Db 2 GAAGCUGUGUCCUGUCA 19
```

## RESULT 6

```
US-11-101-244-1197383
; Sequence 1197383, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
```

; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1197383  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1197383

Query Match 21.3%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 75;  
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGCTCTGTCA 75  
|||||:|:|:|:|:  
Db 2 GAAGCUGUGUCCUGUCA 19

## RESULT 7

US-11-083-784-1197318  
; Sequence 1197318, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1197318  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1197318

Query Match 21.3%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 75;  
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGCTCTGTCA 75  
|||||:|:|:|:|:  
Db 2 GAAGCUGUGUCCUGUCA 19

## RESULT 8

US-11-083-784-1197383  
; Sequence 1197383, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1197383  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1197383

Query Match 21.3%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 75;  
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGCTCTGTCA 75  
|||||:|:|:|:|:  
Db 2 GAAGCUGUGUCCUGUCA 19

## RESULT 9

US-10-310-914A-1373610/c  
; Sequence 1373610, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1373610  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1373610

Query Match 21.3%; Score 16.4; DB 1; Length 22;  
Best Local Similarity 94.4%; Pred. No. 65;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCTCTGTGAG 44  
|||||:|:|:|:|:  
Db 18 TCTGGAGTCTCTGTGAG 1

## RESULT 10

US-10-310-914A-99908/c  
; Sequence 99908, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 99908  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-99908

Query Match 21.0%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 72;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 31 GAGTCCTCTGAGAGGTAAGA 51  
|||||

Db 21 GAGTCCTCTGAGAGGTAAGA 1

Query Match	20.5%	Score 15.8;	DB 1;	Length 21;
Best Local Similarity	89.5%;	Pred. No. 80;		
Matches	17: Conservative	0: Mismatches	2: Indels	0: Gaps

RESULT 14  
US-11-069-908-3819/c  
; Sequence 3819, Application US/11069908  
; Publication No. US20050266432A

Query Match	20.5%	Score 15.8;	DB 1;	Length 22;
Best Local Similarity	89.5%;	Pred. No. 76;		
Matches 17; Conservative	0;	Mismatches 2;	Indels	Gaps

RESULT 15  
US-10-310-914A-1094322/c  
; Sequence 1094322, Application US/10310914A  
; Publication No. US2006000322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kruzat  
; TITLE OF INVENTION: Bioinformatically det  
; TITLE OF INVENTION: uses thereof

**Qy** 31 GAGTCCTCTGAGAGCTAAAGA 51  
||| ||| ||| ||| ||| ||| ||| |||

**Db** 21 GAGTCTTCTGAGAGCTAAAGGA 1

; LENGTH: 23  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 ; US-10-310-914A-591217

**D<sub>b</sub>**      2 CUCUGAGUGGCAAGAACCAG 22  
          | | : | | | | | | | | | |  
30 CUCUGAGUGGCAAGAACCAG 30

Query Match	21.0%	Score 16.2;	DB 1;	Length 23;
Best Local Similarity	76.2%	Pred. No. 65;		
Matches 16: Conservative		2: Mismatches	3: Indels	0: Gaps

RESULT 13  
US-10-972-767-181  
; Sequence 181, Application US/10972767  
; Publication No. US2006008815A1  
; GENERAL INFORMATION:  
; APPLICANT: METAMORPHIX, INC.  
; APPLICANT: Rosenfeld, David  
; APPLICANT: Kerr, Richard  
; APPLICANT: Hutton, Michelle



```
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1094322
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1094322

Query Match      20.3%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

Qy 11 GCCTGGGGATACAACTCTGGA 32
Db 22 GCCCTGGGGATCCAGCCCTGGA 1

RESULT 16
US-11-101-244-826612/c
; Sequence 826612, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 826612
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-826612

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 59 AAGCTGATGTCCTGTCA 75
Db 17 AAGCTGATGTCCTGTCA 1

RESULT 17
US-11-101-244-1197334
; Sequence 1197334, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 826612
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-826612

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 59 AAGCTGATGTCCTGTCA 75
Db 17 AAGCTGATGTCCTGTCA 1

RESULT 18
US-11-101-244-1197395
; Sequence 1197395, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1197395
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1197395

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 98;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCTGTCA 75
Db 1 AAGCUGGUGUCCUGUCA 17

RESULT 19
US-11-101-244-1375618
; Sequence 1375618, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1197395
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1197395

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 98;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCTGTCA 75
Db 1 AAGCUGGUGUCCUGUCA 17
```

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; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1375618
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1375618

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 98;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGTGAGA 43
Db 3 UCUGGAGUCCUGUGUGA 19

RESULT 20
US-11-083-784-826612/c
; Sequence 826612, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 826612
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-826612

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGTCA 75
Db 17 AAGCTGAAGTCTGTCA 1

RESULT 21
US-11-083-784-1197334
; Sequence 1197334, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 826612
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1197334

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 98;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGTCA 75
Db 1 AAGCTGUGUGUCCUGUCA 17

RESULT 22
US-11-083-784-1197395
; Sequence 1197395, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1197395
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1197395

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 98;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGTCA 75
Db 1 AAGCTGUGUGUCCUGUCA 17

RESULT 23
US-11-083-784-1375618
; Sequence 1375618, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
```

; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1375618  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1375618

Query Match 20.0%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 64.7%; Pred. No. 98;  
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCTCTCGAGA 43  
:|||||:|:|:|  
Db 3 UCUGGAGUCCUCUGUGA 19

RESULT 24  
US-10-310-914A-1373632/c  
; Sequence 1373632, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1373632  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1373632

Query Match 20.0%; Score 15.4; DB 1; Length 21;  
Best Local Similarity 94.1%; Pred. No. 89;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCTCTCGAGA 43  
|||||:|:|:|  
Db 17 TCTGGAGTCTCTGTGA 1

RESULT 25  
US-10-310-914A-820857  
; Sequence 820857, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 820857  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-820857

Query Match 19.7%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 98;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 42 GAGGTAAGAGCCAGCGAAG 61  
|||||:|:|:|  
Db 1 GAGGTAAGAGCCAGCGAAG 20

RESULT 26  
US-10-310-914A-946704/c  
; Sequence 946704, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 946704  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-946704

Query Match 19.7%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 93;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 42 GAGGTAAGAGCCAGCGAAG 61  
|||||:|:|:|  
Db 20 GAGGTAAGAGCCAGCGAG 1

RESULT 27  
US-10-310-914A-1213419  
; Sequence 1213419, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1213419  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1213419

Query Match 19.5%; Score 15; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 26 CTCTGGAGTCTCTG 40  
:|:|:|:|:|:|  
Db 2 CUCUGGAGUCCUCUG 16

RESULT 28  
US-10-310-914A-45021  
; Sequence 45021, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 45021  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-45021

Query Match 19.2%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.2e+02;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGCTGGGGATACAATC 28  
|||||:||||:|||||  
Db 1 GGGCUGGGGACACAC 18

RESULT 29  
US-10-310-914A-921346  
Sequence 921346, Application US/10310914A  
Publication No. US2006000322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiler, Kvazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 921346  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-921346

Query Match 19.2%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 77.8%; Pred. No. 1.2e+02;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGCTGGGGATACAATC 28  
|||:|||||:|||||  
Db 1 GGGCUGGGGACACAC 18

RESULT 30  
US-10-310-914A-946718/c  
Sequence 946718, Application US/10310914A  
Publication No. US2006000322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiler, Kvazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 946718  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-946718

Query Match 19.2%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 42 GAGGTAAAGAGCCAGCGA 59  
|||||:|||||:|||||  
Db 18 GAGGGAGAGAGCCAGCGA 1  
RESULT 31  
US-10-310-914A-1358783/c  
Sequence 1358783, Application US/10310914A  
Publication No. US2006000322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiler, Kvazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1358783  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1358783

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAGCTG 64  
|||||:|||||:|||||  
Db 18 AAAGAGCCAGCGAAGCTG 1

RESULT 32  
US-11-101-244-446294/c  
Sequence 446294, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmoon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 446294  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-446294

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 CTCGGAGTCTCTGAGA 43  
|||||:|||||:|||||  
Db 18 CTCGGAGTCTCTGATA 1

## RESULT 33

US-11-101-244-462186  
; Sequence 462186, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 462186  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-462186

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 21 TACAACCTGGAGTCCTC 38  
:||||| |:|||||:|  
Db 2 UACAACACUGAGUCAUC 19

## RESULT 34

US-11-101-244-673763  
; Sequence 673763, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 673763  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-673763

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 61.1%; Pred. No. 1.1e+02;  
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 60 AGCTGATGTCCTGTCAAG 77  
||||| |:|:|:|  
Db 2 AGCUGUGUUCUGUCAAG 19

## RESULT 35

US-11-101-244-741998

US-11-101-244-686604  
; Sequence 686604, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 686604  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-686604

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 47 AAAGAGCCGAGGAGCTG 64  
||||| |:|||||:|  
Db 2 AAAGAGCCGAGGAGCAUG 19

## RESULT 36

US-11-101-244-716743/C  
; Sequence 716743, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 716743  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-716743

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 25 ACTCTGGAGTCCTCTGAG 42  
||||| |:|:|:|  
Db 19 ACTCTGGAGTCCTCTGAG 2

; Sequence 741998, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR FILING DATE: 2005-02,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 741998  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-741998

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 42 GAGTAAAGAGCCAGCGA 59  
|||||:|||||:|||||  
Db 2 GAGGUAAGGCCAGUGA 19

## RESULT 38

US-11-101-244-1221841  
; Sequence 1221841, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR FILING DATE: 2005-02,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1221841  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1221841

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 54 CAGCGAAGCTGATGTCCT 71  
|||||:|||||:|||||  
Db 1 CAGAGAAGCGUGUGUCCU 18

## RESULT 39

US-11-101-244-1221940  
; Sequence 1221940, Application US/11101244

; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR FILING DATE: 2005-02,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1221940  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1221940

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 54 CAGCGAAGCTGATGTCCT 71  
|||||:|||||:|||||  
Db 1 CAGAGAAGCGUGUGUCCU 18

## RESULT 40

US-11-101-244-1222038  
; Sequence 1222038, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR FILING DATE: 2005-02,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1222038  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1222038

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 54 CAGCGAAGCTGATGTCCT 71  
|||||:|||||:|||||  
Db 1 CAGAGAAGCGUGUGUCCU 18

## RESULT 41

US-11-083-784-446294/c  
; Sequence 446294, Application US/11083784  
; Publication No. US20050245475A1

GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 446294  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-446294

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 26 CTCGGAGTCTCTGACA 43  
DB 18 CTCGGAGTCTCTGATA 1

## RESULT 42

US-11-083-784-462186  
; Sequence 462186, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 462186  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-462186

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 21 TACAACCTCTGGAGTCCTC 38  
DB 2 UACACACUGGAGUCAUC 19

## RESULT 43

US-11-083-784-673763  
; Sequence 673763, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 673763  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-673763

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 61.1%; Pred. No. 1.1e+02;  
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 60 AGCTGATGCTCTGCAAG 77  
DB 2 AGCUGGUGUCUGCAAG 19

## RESULT 44

US-11-083-784-686604  
; Sequence 686604, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 686604  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-686604

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 47 AAGAGCCGCGAGCTG 64  
DB 2 AAGAGCCGCGAACAUG 19

```
RESULT 45
US-11-083-784-716743/C
; Sequence 716743, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 716743
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-716743

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      25 ACTCTGGAGRCCTGTGAG 42
Db      19 ACTCTGGACTCCTGTGAG 2

RESULT 46
US-11-083-784-741998
; Sequence 741998, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 741998
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-741998

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      42 GAGGTAAGAGCCAGCGA 59
Db      2 GAGGTAAGAGCCAGUGA 19

RESULT 47
US-11-083-784-1221841
; Sequence 1221841, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1221841
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1221841

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      54 CAGCGAAGCTGATGTCCT 71
Db      1 CAGAGAAGCUGUGUCCU 18

RESULT 48
US-11-083-784-1221940
; Sequence 1221940, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1221940
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1221940

Query Match      19.2%; Score 14.8; DB 1; Length 19;
```



Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 54 CAGCGAAGCTGATCTCT 71  
||| |||||:|:|:|:  
Db 1 CAGAGAAGCUGCUGUCCU 18

## RESULT 49

US-11-083-784-1222038  
; Sequence 1222038, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR FILING DATE: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1222038  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1222038

Query Match 19.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 54 CAGCGAAGCTGATCTCT 71  
||| |||||:|:|:|:  
Db 1 CAGAGAAGCUGCUGUCCU 18

## RESULT 50

US-10-310-914A-1045625/c  
; Sequence 1045625, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1045625  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1045625

Query Match 19.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 15 TGGGGATACCACTCTGGA 32  
|||||||:|:|:|:  
Db 19 TGGGGATACCACTCTGGA 2

## RESULT 51

US-10-310-914A-144915/c  
; Sequence 144915, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 144915  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-144915

Query Match 18.7%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACAAGACGGCTGGG 19  
|||||:|:|:|:  
Db 18 ACAAGACGGCTGGG 3

## RESULT 52

US-11-101-244-527885/c  
; Sequence 527885, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 527885  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-527885

Query Match 18.7%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATCTCTGT 73  
|||||:|:|:|:  
Db 18 GAATCTGATCTCTGT 3

## RESULT 53

US-11-101-244-681299  
; Sequence 681299, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.



```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1323244
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1323244

```

```

Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 68.8%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 28 CTGGAGTCCTCTGAGA 43
Db 2 CUGGACUCCUCUGAGA 17

```

```

RESULT 58
US-11-101-244-1435551/c
; Sequence 1435551, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1435551
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1435551

```

```

Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 27 TCTGGAGTCCTCTGAG 42
Db 17 TCTGGAGACCTCTGAG 2

```

```

RESULT 59
US-11-101-244-1526025/c
; Sequence 1526025, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1526025
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1526025

```

```

Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 26 CTCGGAGTCCTCTGA 41
Db 16 CTCGGAGTACTCTGA 1

```

```

RESULT 60
US-11-101-244-1526053/c
; Sequence 1526053, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1526053
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1526053

```

```

Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 26 CTCGGAGTCCTCTGA 41
Db 18 CTCGGAGTACTCTGA 3

```

```

RESULT 61
US-11-083-784-527885/c
; Sequence 527885, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 527885
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-527885

Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      58 GAAGCTGATGTCCTGT 73
Db      18 GAATCTGATGTCCTGT 3

RESULT 62
US-11-083-784-681299
; Sequence 681299, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 681299
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-681299

Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      22 ACAACTCTGGAGTCCT 37
Db      3 ACAACUCUGGAGUCCU 18

RESULT 63
US-11-083-784-1025484/c
; Sequence 1025484, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1025484
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1025484

Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 68.8%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      22 ACAACTCTGGAGTCCT 37
Db      3 ACAACUCUGGAGUCCU 18

RESULT 64
US-11-083-784-1155118
; Sequence 1155118, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1155118
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1155118

Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 68.8%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      22 ACAACTCTGGAGTCCT 37
Db      3 ACAACUCUGGAGUCCU 18

RESULT 65
US-11-083-784-1256070/c
; Sequence 1256070, Application US/11083784
; Publication No. US20050245475A1
; APPLICANT: Khvorova, Anastasia
```

GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR FILING DATE: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1256070  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-1256070

Query Match 18.7%; Score 14.4; DB 1; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGCGAAGC 62  
 Db 18 AAAGAGCCAGTGAAGC 3

## RESULT 66

US-11-083-784-1323244  
 ; Sequence 1323244, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR FILING DATE: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1323244  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-1323244

Query Match 18.7%; Score 14.4; DB 1; Length 19;  
 Best Local Similarity 68.8%; Pred. No. 1.3e+02;  
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGAGTCTCTGAGA 43  
 Db 2 CUGGACUCCUGAGA 17

## RESULT 67

US-11-083-784-1323244

US-11-083-784-1435551/c  
 ; Sequence 1435551, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR FILING DATE: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1435551  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-1435551

Query Match 18.7%; Score 14.4; DB 1; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCTCTGAG 42  
 Db 17 TCTGGAGCTCTGAG 2

## RESULT 68

US-11-083-784-1526025/c  
 ; Sequence 1526025, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR FILING DATE: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1526025  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-1526025

Query Match 18.7%; Score 14.4; DB 1; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 26 CTCTGGAGTCTCTGA 41  
 Db 16 CTCTGGAGTCTCTGA 1

## RESULT 69

US-11-083-784-1526053/c

; Sequence 1526053, Application US/11083784

; Publication No. US20050245475A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13498US

; CURRENT APPLICATION NUMBER: US/11/083,784

; CURRENT FILING DATE: 2005-03-18

; PRIOR APPLICATION NUMBER: US/10/714,333

; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 159111

; SOFTWARE: Proprietary

; SEQ ID NO 1526053

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

; US-11-083-784-1526053

Query Match 18.7%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 1.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 CTCCTGGAGTCTCTGA 41

Db 18 CTCCTGGAGTCTCTGA 3

## RESULT 70

US-10-750-185-15591/c

; Sequence 15591, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 15591

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Forward Primer

US-10-750-185-15591

Query Match 18.7%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 1.2e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 AACTCTGGAGTCTCTCT 39

Db 20 AACTCTGGAGTCTCT 5

## RESULT 71

US-10-750-623-15591/c

; Sequence 15591, Application US/10750623

; Publication No. US20050287531A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-1

; CURRENT APPLICATION NUMBER: US/10/750,623

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 15591

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Forward Primer

US-10-750-623-15591

Query Match 18.7%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 1.2e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 AACTCTGGAGTCTCTCT 39

Db 20 AACTCTGGAGTCTCTCT 5

## RESULT 72

US-10-310-914A-562241/c

; Sequence 562241, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 562241

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-562241

Query Match 18.4%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 1.3e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 35 CCTCTGAGAGGTAAAGAGC 53

Db 19 CCGCTGAGTGGCAAGAGC 1

## RESULT 73

US-10-310-914A-1111642/c

; Sequence 1111642, Application US/10310914A

```

; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1111642
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1111642

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      25  ACTCTGGAGTCTCTGAGA 43
      ||||| ||||| |||||
Db      19  ACCCTGGACCTCTGAGA 1

RESULT 74
US-11-101-244-197226
; Sequence 197226, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 197226
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-197226

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      50  GAGCCAGCGAGCTGATGT 68
      ||||| ||||| |||||
Db      1  GGGCCAGGUNGUGUGUGU 19

RESULT 75
US-11-101-244-404601/c
; Sequence 404601, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 404601
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-404601

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      18  GGATACAACTCTGGAGTCC 36
      ||||| ||||| |||||
Db      19  GAATACAAATCTGGAATCC 1

RESULT 76
US-11-101-244-518286/c
; Sequence 518286, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 518286
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-518286

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      20  ATACAACTCTGGAGTCTCTC 38
      ||||| ||||| |||||
Db      19  ATACAACTCTGCTCTCTCTC 1

RESULT 77
US-11-101-244-527824/c
; Sequence 527824, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

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; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 527824
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-527824

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 51 AGCCAGCGAAGCTGATGTC 69
   ||||| ||||| ||||| |||||
Db 19 AACCAGTGATCTGATGTC 1

RESULT 78
US-11-101-244-539604
; Sequence 539604, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 539604
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-539604

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 42 GAGGTAAGAGCCAGCGAA 60
   ||||| ||||| ||||| |||||
Db 1 GAGGTAAGAGCUCAGCUAA 19

RESULT 79
US-11-101-244-618922
; Sequence 618922, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 618922
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-618922

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCTCTCTGA 41
   ||||| ||||| ||||| |||||
Db 19 CTACTCTGGACTCTCTGTGA 1

RESULT 80
US-11-101-244-716725/c
; Sequence 716725, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 716725
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-716725

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCTCTCTGA 41
   ||||| ||||| ||||| |||||
Db 19 CTACTCTGGACTCTCTGTGA 1

RESULT 81
US-11-101-244-749629/c
; Sequence 749629, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
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; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 749629
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-749629

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 34 TCCTCTGAGAGGTTAAAGAG 52
Db 19 TCCTCTTAGAGGTACAGAG 1

RESULT 82
US-11-101-244-819751
; Sequence 819751, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 819751
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-819751

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 30 GGAGTCTCTGAGAGGTAA 48
Db 1 GGAGAGUCUGAGAGGUA 19

RESULT 83
US-11-101-244-840452
; Sequence 840452, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07

; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 840452
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-840452

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 42 GAGGTAAGAGCCGAGCGAA 60
Db 1 GAGGTAAGAGCCGAGGAA 19

RESULT 84
US-11-101-244-931449
; Sequence 931449, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 931449
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-931449

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 47 AAAGAGCCGAGCGAAGCTGA 65
Db 1 AAAGAGCCCAUCCAGGCUAA 19

RESULT 85
US-11-101-244-1006983/c
; Sequence 1006983, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07

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; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1006983
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1006983

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCTCTGA 41
Db 19 CAAATCTGGAGTCTCTTA 1

RESULT 86
US-11-101-244-1178034/c
; Sequence 1178034, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1178034
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1178034

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAACAGACGGCTGGG 19
Db 19 CAATCATGACGGCTGGT 1

RESULT 87
US-11-101-244-1238798
; Sequence 1238798, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1238798
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1238798

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCTCTGA 41
Db 19 CATCTCTGGAGTCAGCTGA 1

RESULT 88
US-11-101-244-1257649/c
; Sequence 1257649, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1257649
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1257649

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCTCTGA 41
Db 19 CATCTCTGGAGTCAGCTGA 1

RESULT 89
US-11-101-244-1286557/c
; Sequence 1286557, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286557
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1286557
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<p>; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 1402806 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-1286557</p>	<p>Query Match 18.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 1.3e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>	<p>QY 56 GCAGGCTGATGTCTGTC 74           DB 19 GTGAAGTGAAGTCTGTC 1</p>
RESULT 90		
<p>US-11-101-244-1327450/c ; Sequence 1327450, Application US/11101244 ; Publication No. US20050246794A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmacon, Inc. ; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101.244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 1327450 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-1327450</p>	<p>Query Match 18.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 1.3e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>	<p>QY 54 CAGCGAGCTGATGTCTGTC 72           DB 19 CAATGAGCTGAGTCTGTC 1</p>
RESULT 91		
<p>US-11-101-244-1402806/c ; Sequence 1402806, Application US/11101244 ; Publication No. US20050246794A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmacon, Inc. ; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101.244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14</p>	<p>Query Match 18.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 1.3e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>	<p>QY 34 TCCTCTGAGAGTTAAAGAG 52           DB 19 TTCTTTGAGAGTTAAGGAG 1</p>
RESULT 92		
<p>US-11-101-244-1508424/c ; Sequence 1508424, Application US/11101244 ; Publication No. US20050246794A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmacon, Inc. ; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101.244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 1508424 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-1508424</p>	<p>Query Match 18.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 1.3e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>	<p>QY 34 TCCTCTGAGAGTTAAAGAG 52           DB 19 TTCTTTGAGAGTTAAGGAG 1</p>
RESULT 93		
<p>US-11-083-784-197226 ; Sequence 197226, Application US/11083784 ; Publication No. US20050245475A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmacon, Inc. ; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/083,784 ; CURRENT FILING DATE: 2005-03-18 ; PRIOR APPLICATION NUMBER: US/10/714,333 ; PRIOR FILING DATE: 2003-11-14 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137</p>	<p>Query Match 18.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 1.3e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>	<p>QY 34 TCCTCTGAGAGTTAAAGAG 52           DB 19 TTCTTTGAGAGTTAAGGAG 1</p>

```
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 197226
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-197226

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAAGCTGATGT 68
Db 1 GGGCCAGAGUGGUGAUGU 19

RESULT 94
US-11-083-784-404601/c
; Sequence 404601, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 404601
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-404601

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTCC 36
Db 19 GAATACAAATCTGGAATCC 1

RESULT 95
US-11-083-784-518286/c
; Sequence 518286, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 518286
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-518286

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 51 AGCCAGCGAAGCTGATGTC 69
Db 19 AACCACTGATCTGATGTC 1

RESULT 97
US-11-083-784-539604
; Sequence 539604, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 527824
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-527824

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 20 ATACAACCTCTGGAGTCTC 38
Db 19 ATACAACCTCTGCTCTCCTC 1

RESULT 96
US-11-083-784-527824/c
; Sequence 527824, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 527824
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-527824

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 20 ATACAACCTCTGGAGTCTC 38
Db 19 ATACAACCTCTGCTCTCCTC 1
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; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 539604
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-539604

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 42 GAGTAAAGCCGACGGA 60
    ||||:|||||
Db 1 GAGGUAAGCUCACGCUAA 19

RESULT 98
US-11-083-784-618922
; Sequence 618922, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 618922
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-618922

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 1.3e+02;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 25 ACTCTGAGTCCTCTGAGA 43
    |:|:|:|:|:|:|
Db 1 AAUCUUGAGUCUUCUGAGA 19

RESULT 99
US-11-083-784-716725/c
; Sequence 716725, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

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; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 716725
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-716725

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 23 CAACCTCGAGTCCTCTGA 41
    |||||:|||||
Db 19 CTACTCTGGACTCCTCTGGA 1

RESULT 100
US-11-083-784-749629/c
; Sequence 749629, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 749629
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-749629

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 34 TCCTCTGAGAGGTAAGAG 52
    |||||:|||||
Db 19 TCTTCTTAGAGGTACAGAG 1

RESULT 101
US-11-083-784-819751
; Sequence 819751, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela

```

; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 819751  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-819751

Query Match 18.4%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 1.3e+02;  
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 30 GGAGTCTCTGAGAGGTAA 48  
|||||:|||||:  
Db 1 GGAGAGCUCGAGAGGUA 19

RESULT 102  
US-11-083-784-840452  
; Sequence 840452, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 840452  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-840452

Query Match 18.4%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 42 GAGTAAAGCAGCGCAA 60  
|||||:  
Db 1 GAGGAAAGCAGAGAA 19

RESULT 103  
US-11-083-784-931449  
; Sequence 931449, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 931449  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-931449

Query Match 18.4%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 1.3e+02;  
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 47 AAAGAGCCAGCGAAGCTGA 65  
|||||:  
Db 1 AAAGAGCCAUCCAAGCUAA 19

RESULT 104  
US-11-083-784-1006983/c  
; Sequence 1006983, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1006983  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1006983

Query Match 18.4%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 23 CAACTCTGGAGTCTCTGA 41  
|||||:  
Db 19 CAAATCTGGAGTCTCTTA 1

RESULT 105  
US-11-083-784-1178034/c

```

; Sequence 1178034, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1178034
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1178034

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACAAGACGGCTGGG 19
DB 19 CAATCATGACGGCTGGT 1

RESULT 106
US-11-083-784-1238798
; Sequence 1238798, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1238798
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1238798

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 1.3e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACCTCGAGTCTCTGGA 41
DB 1 CAACUCUGGAGUCUUCUGA 19

RESULT 107
US-11-083-784-1257649/c
; Sequence 1257649, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1257649
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1257649

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACCTCGAGTCTCTGGA 41
DB 19 CATCTCGAGTCAGCTGA 1

RESULT 108
US-11-083-784-1286557/c
; Sequence 1286557, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286557
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1286557

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.3%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 56 GCGAAGCTGATGTCCTGTC 74

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Db 19 GTGAAGATGAAGTCTCTGTC 1  
 |||||  
 RESULT 109  
 US-11-083-784-1327450/c  
 ; Sequence 1327450, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; PRIOR FILING DATE: 2005-03-18  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1327450  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-1327450  
 Query Match 18.4%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 54 CAGCGAAGTGTGATGTCCTG 72  
 |||||  
 Db 19 CAATGAAGTGAAGTCTCTG 1  
 |||||  
 RESULT 110  
 US-11-083-784-1402806/c  
 ; Sequence 1402806, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; PRIOR FILING DATE: 2005-03-18  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1402806  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-1402806  
 Query Match 18.4%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 54 CAGCGAAGTGTGATGTCCTG 72  
 |||||  
 Db 19 CAATGAAGTGAAGTCTCTG 1  
 |||||  
 RESULT 111  
 US-11-083-784-1508424/c  
 ; Sequence 1508424, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; PRIOR FILING DATE: 2005-03-18  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1508424  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-1508424  
 Query Match 18.4%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 23 CAAATCTGAGTCTCTCTGA 41  
 |||||  
 Db 19 CAAATCTGAATTCCTCTGA 1  
 |||||  
 RESULT 112  
 US-10-310-914A-128507/c  
 ; Sequence 128507, Application US/10310914A  
 ; Publication No. US2006000332A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shiler, Kvuzat  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory g  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 128507  
 ; LENGTH: 20  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-128507  
 Query Match 18.4%; Score 14.2; DB 1; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 41 AGAGGTAAGAGCCGCGA 59  
 |||||  
 Db 20 AGAGGGAGGAGCGGCGA 2  
 |||||



```
RESULT 113
US-10-310-914A-658051/c
; Sequence 658051, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 658051
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-658051

Query Match      18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      15 TGGGATACACTCTGGAG 33
Db      20 TGGGATTCAGCTCTAGAG 2

RESULT 114
US-10-310-914A-833580/c
; Sequence 833580, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 833580
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-833580

Query Match      18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      38 CTGAGAGGTAAGGCCAG 56
Db      20 CTCAGAGGAAAGGCCAG 2

RESULT 115
US-10-310-914A-971008/c
; Sequence 971008, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
```

```
; SEQ ID NO 971008
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-971008

Query Match      18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      40 GAGAGGTAAGGCCAGCG 58
Db      20 GAGAGCCAGAGCCAGCG 2

RESULT 116
US-10-310-914A-1087873
; Sequence 1087873, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1087873
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1087873

Query Match      18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 68.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      36 CTCGAGAGGTAAGGCC 54
Db      1 CUCGAGAGGCUAAGUGAC 19

RESULT 117
US-10-310-914A-1313685/c
; Sequence 1313685, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1313685
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1313685

Query Match      18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      34 TCCTCTGAGAGGTAAGAG 52
Db      20 TTCTGTGAGAGGAAAGAG 2
```



; SEQ ID NO 43662  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-43662

Query Match 18.2%; Score 14; DB 1; Length 20;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 64 GATGTCCTGTCAG 77  
||:|:|:|:|:|:|  
Db 4 GAUGUCUGCAAG 17

## RESULT 123

US-10-310-914A-732261  
; Sequence 732261, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087, 0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 732261  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-732261

Query Match 17.9%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 76.5%; Pred. No. 1.6e+02;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAGCTGAT 66  
|||||:|:|:|:|:  
Db 1 GAGCCAGCGAGCTGCU 17

## RESULT 124

US-10-310-914A-815753/c  
; Sequence 815753, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087, 0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 815753  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-815753

Query Match 17.9%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GAGCGCTGGGGATACA 24  
||:|:|:|:|:|:|  
Db 17 GCGCGCTGGGGGTACA 1

## RESULT 125

US-10-310-914A-946707/c  
; Sequence 946707, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087, 0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 946707  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-946707

Query Match 17.9%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 43 AGCTAAGAGCCAGCGA 59  
||:|:|:|:|:|:|  
Db 18 AGGAGAGAGCCAGCGA 2

## RESULT 126

US-10-310-914A-202536  
; Sequence 202536, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087, 0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 202536  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-202536

Query Match 17.9%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 82.4%; Pred. No. 1.5e+02;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 48 AAGAGCCAGCGAGCTG 64  
||:|:|:|:|:|:|  
Db 3 AAGAGAGAGGGAAGCUG 19

## RESULT 127

US-10-310-914A-760173/c  
; Sequence 760173, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087, 0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 760173

```
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-760173

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAACAAGACGGCTGGG 18
Db 17 AAATAAGATGGCTGGG 1

RESULT 128
US-10-310-914A-785948
; Sequence 785948, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 785948
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-785948

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGCTGGGGATACACT 27
Db 3 GGCCUGGGGACACAGCU 19

RESULT 129
US-10-310-914A-1194348
; Sequence 1194348, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1194348
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1194348

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 28 CTGGAGTCCTCTGAGAG 44
Db 2 CUUGUGUCCUCUGAGAG 18

RESULT 130
```

```
US-11-101-244-14272
; Sequence 14272, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 14272
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-14272

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTGTC 74
Db 2 GAAGUCGAGUCCUGUC 18

RESULT 131
US-11-101-244-67079
; Sequence 67079, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 67079
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-67079

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 28 CTGGAGTCCTCTGAGAG 44
Db 2 CUGGAGUCUCCUGAGAG 18

RESULT 132
US-11-101-244-98224/c
```

```
; Sequence 98224, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 98224
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-98224

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTGTC 74
DB 17 GAAGGTGATGTCCTGGC 1

RESULT 133
US-11-101-244-160889
; Sequence 160889, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 160889
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-160889

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGCTCTGT 73
DB 1 CGAAGGGGAUGUCCUGU 17

RESULT 134
US-11-101-244-160989
; Sequence 160989, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 160989
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-160989

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGCTCTGT 73
DB 1 CGAAGGGGAUGUCCUGU 17

RESULT 135
US-11-101-244-161088
; Sequence 161088, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 161088
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-161088

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGCTCTGT 73
DB 1 CGAAGGGGAUGUCCUGU 17

RESULT 136
US-11-101-244-161190
; Sequence 161190, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 161190
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-161190

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGCTCTGT 73
DB 1 CGAAGGGGAUGUCCUGU 17
```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 161190
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-161190

```

```

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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```

Qy 57 CGAAGCTGATGCTCTGT 73
Db 1 CGAAGGGGAGUGCCUGU 17

```

```

RESULT 137
US-11-101-244-197189
; Sequence 197189, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 197189
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-197189

```

```

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 52 GCCAGCGAGCTGATGT 68
Db 2 GCCAGAGGAGUGCCUGU 18

```

```

RESULT 138
US-11-101-244-219953
; Sequence 219953, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 219953
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-219953

```

```

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 37 TCTGAGAGGTAAAGAGC 53
Db 1 UCUGAAGAGUAAAGAGC 17

```

```

RESULT 139
US-11-101-244-276299
; Sequence 276299, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 276299
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-276299

```

```

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 16 GGGGATACAACTCTGGA 32
Db 2 GAGGAUACAGCUCUGGA 18

```

```

RESULT 140
US-11-101-244-290226
; Sequence 290226, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.

```

; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 290226  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-290226

Query Match 17.9%; Score 13.8; DB 1; Length 19;  
 Best Local Similarity 82.4%; Pred. No. 1.5e+02;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCGCGAA 60  
 ||:||||| ||| |||  
 Db 2 GGUAAGAGUCAGAGAA 18

RESULT 141  
 US-11-101-244-290240  
 ; Sequence 290240, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 290240  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-290240

Query Match 17.9%; Score 13.8; DB 1; Length 19;  
 Best Local Similarity 82.4%; Pred. No. 1.5e+02;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCGCGAA 60  
 ||:||||| ||| |||  
 Db 1 GGUAAGAGUCAGAGAA 17

RESULT 142  
 US-11-101-244-40405/c  
 ; Sequence 40405, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 40405  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-40405

Query Match 17.9%; Score 13.8; DB 1; Length 19;  
 Best Local Similarity 88.2%; Pred. No. 1.5e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 37 TCTGAGAGGTAAAGAC 53  
 ||||| ||| |||||  
 Db 17 TCTGAGGATAAAGAC 1

RESULT 143  
 US-11-101-244-440203  
 ; Sequence 440203, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 440203  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-440203

Query Match 17.9%; Score 13.8; DB 1; Length 19;  
 Best Local Similarity 88.2%; Pred. No. 1.5e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAACAAGACGGCTGGG 18  
 ||||| ||||| |||  
 Db 1 AAACAAGACGGCGUGG 17

RESULT 144  
 US-11-101-244-524859  
 ; Sequence 524859, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela





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; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 731099
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-731099

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      24  AACTCTGGAGTCCTCTG 40
      ||||| |||||
Db      18  AACTCTGAATTCCTCTG 2

RESULT 149
US-11-101-244-731168/c
; Sequence 731168, Application US/11/101.244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 731168
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-731168

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      24  AACTCTGGAGTCCTCTG 40
      ||||| |||||
Db      17  AACTCTGAATTCCTCTG 1

RESULT 150
US-11-101-244-751095/c
; Sequence 751095, Application US/11/101.244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

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; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 751095
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-751095

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      35  CCTCTGAGAGGTAAGA 51
      ||||| |||||
Db      18  CTCTGAGAGGTAACA 2

RESULT 151
US-11-101-244-813171/c
; Sequence 813171, Application US/11/101.244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 813171
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-813171

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      21  TACAACCTCTGGAGTCCT 37
      ||||| |||||
Db      19  TACAGCTCTGGAGTCCT 3

RESULT 152
US-11-101-244-862664/c
; Sequence 862664, Application US/11/101.244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

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; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 862664
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-862664

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 ACTCTGGAGTCTCTCTGA 41
Db 17 ACACCGAGTCTCTCTGA 1

RESULT 153
US-11-101-244-900906
; Sequence 900906, Application US/11/101,244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 900906
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-900906

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 38 CTGAGAGGTTAAGAGCC 54
Db 2 CUGAGAGCUAAGAGAC 18

RESULT 154
US-11-101-244-941347/c
; Sequence 941347, Application US/11/101,244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 941347
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-941347

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCTGAGA 43
Db 19 TCTTGAGTCCACTGAGA 3

RESULT 155
US-11-101-244-959690
; Sequence 959690, Application US/11/101,244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 959690
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-959690

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGTCCT 71
Db 2 AGUGAAGCUGAUGUUCU 18

RESULT 156
US-11-101-244-966428
; Sequence 966428, Application US/11/101,244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
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; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 966428
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-966428

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.2%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAACAAGAGCGGCGCTGG 17
Db 1 CAAACAAGAGACCCUGG 17

RESULT 157
US-11-101-244-1036369
; Sequence 1036369, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1036369
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1036369

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 45 GTAAAGAGCCGCGCAAG 61
Db 1 GCAAAGAGCGCGCAAG 17

RESULT 158
US-11-101-244-1069062/c
; Sequence 1069062, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07

; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1069062
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1069062

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGCGCAAGC 62
Db 19 TAAATGCCGCGCGAAGC 3

RESULT 159
US-11-101-244-1149570
; Sequence 1149570, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1149570
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1149570

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 60 AGCTGATGTCCTGTCAC 76
Db 2 AGAUGAUGUCCUGGCA 18

RESULT 160
US-11-101-244-1271626
; Sequence 1271626, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07

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; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1271626
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1271626

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.2%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTGTC 74
Db 2 GAGGCAGAUCCUGUC 18

RESULT 161
US-11-101-244-1286508/c
; Sequence 1286508, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286508
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1286508

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTGTC 74
Db 18 GAAGATGAAGTCTCTGTC 2

RESULT 162
US-11-101-244-1286517/c
; Sequence 1286517, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286517
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1286517

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGCTCCT 71
Db 18 AGCAAGATGATGACCT 2

RESULT 163
US-11-101-244-1299503/c
; Sequence 1299503, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1299503
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1299503

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGCTCCT 71
Db 18 AGCAAGATGATGACCT 2

RESULT 164
US-11-101-244-1321159
; Sequence 1321159, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1321159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1321159

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGCTCCT 71
Db 18 AGCAAGATGATGACCT 2
```

```
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1321159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1321159

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGAGT 34
   ||:||||| |:|||||
Db 1 GGATACAACTCTGAGT 17

RESULT 165
US-11-101-244-1334132
; Sequence 1334132, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1334132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1334132

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 35 CCTCTGAGAGTAAAGA 51
   ||:||||| |:|||||
Db 1 CCUCUGAGAGUCAAGA 17

RESULT 166
US-11-101-244-1359524
; Sequence 1359524, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359524
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1359524

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 44 GGTAAAGAGCCAGCGAA 60
   |:||||| |:|||||
Db 1 GAUAAAGAGUCAGCGAA 17

RESULT 167
US-11-101-244-1359621
; Sequence 1359621, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359621
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1359621

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 44 GGTAAAGAGCCAGCGAA 60
   |:||||| |:|||||
Db 1 GAUAAAGAGUCAGCGAA 17

RESULT 168
US-11-101-244-1453192/c
; Sequence 1453192, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1453192/c
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1453192/c

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 44 GGTAAAGAGCCAGCGAA 60
   |:||||| |:|||||
Db 1 GAUAAAGAGUCAGCGAA 17
```

```
; SOFTWARE: Proprietary
; SEQ ID NO 1453192
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1453192

Query Match          17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGTCCT 71
Db 18 AGAGAAGATGATGTCCT 2

RESULT 169
US-11-101-244-1510975
; Sequence 1510975, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1510975
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1510975

Query Match          17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 45 GTAAAGAGCCAGCGAAG 61
Db 1 GUGAAGAGCCAGUGAAG 17

RESULT 170
US-11-101-244-1565567/c
; Sequence 1565567, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

; SEQ ID NO 1565567
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1565567

Query Match          17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAGCT 63
Db 18 AATGAGCCAGCGAAGAT 2

RESULT 171
US-11-083-784-14272
; Sequence 14272, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 14272
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-14272

Query Match          17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTGTC 74
Db 2 GAAGUCGAUGUCCUGUC 18

RESULT 172
US-11-083-784-67079
; Sequence 67079, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; SOFTWARE: Proprietary
```

```
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 67079
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-67079

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      28 CTGAGCTCCTGACAG 44
      |:|:|:|:|:|:|:|:|
Db      2 CUGGAGUCUCUGACAG 18

RESULT 173
US-11-083-784-98224/c
; Sequence 98224, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 98224
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-98224

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      58 GAAGCTGATGTCCTGTC 74
      ||||| ||||| |||||
Db      17 GAAGTGTATGTCCTGGC 1

RESULT 174
US-11-083-784-160889
; Sequence 160889, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 160889
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-160889

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      57 CGAAGCTGATGTCCTGT 73
      ||||| ||||| |||||
Db      1 CGAAGGGGAGUCCUGU 17

RESULT 175
US-11-083-784-160989
; Sequence 160989, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 160989
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-160989

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      57 CGAAGCTGATGTCCTGT 73
      ||||| ||||| |||||
Db      1 CGAAGGGGAGUCCUGU 17

RESULT 176
US-11-083-784-161088
; Sequence 161088, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
```

Query Match	Best Local Similarity	Score	DB 1	Length	Indels	Mismatches	Gaps
Query Match	Best Local Similarity	Score	DB 1	Length	Indels	Mismatches	Gaps
Matches 12; Conservative	Matches 12; Conservative	3; Mismatches	2; Indels	0; Gaps	0;	0;	0;
Qy	52	GCCAGCGAGCTGATGT	68				
Db	2	GCCAGAGUAGCUGAUGU	18				
RESULT 179	US-11-083-784-219953	Sequence 219953, Application US/11083784					
	Publication No. US20050245475A1	GENERAL INFORMATION:					
	APPLICANT: Dharmacon, Inc.	APPLICANT: Khvorova, Anastasia					
	APPLICANT: Reynolds, Angela	APPLICANT: Marshall, William					
	APPLICANT: Scaringe, Stephen	APPLICANT: Scaringe, Stephen					
	FILE REFERENCE: 13499US	TITLE OF INVENTION: Functional and Hyperfunctional siRNA					
	CURRENT APPLICATION NUMBER: US/11/083,784	CURRENT FILING DATE: 2005-03-18					
	PRIOR APPLICATION NUMBER: US/10/714,333	PRIOR FILING DATE: 2003-11-14					
	PRIOR APPLICATION NUMBER: 60/502,050	PRIOR FILING DATE: 2003-09-10					
	PRIOR APPLICATION NUMBER: 60/426,137	PRIOR FILING DATE: 2002-11-14					
	NUMBER OF SEQ ID NOS: 1591911	SOFTWARE: Proprietary					
	SEQ ID NO 161190	LENGTH: 19					
	TYPE: RNA	ORGANISM: Homo sapiens					
	US-11-083-784-161190	Sequence 161190, Application US/11083784					
	Publication No. US20050245475A1	GENERAL INFORMATION:					
	APPLICANT: Dharmacon, Inc.	APPLICANT: Khvorova, Anastasia					
	APPLICANT: Reynolds, Angela	APPLICANT: Marshall, William					
	APPLICANT: Scaringe, Stephen	APPLICANT: Scaringe, Stephen					
	FILE REFERENCE: 13499US	TITLE OF INVENTION: Functional and Hyperfunctional siRNA					
	CURRENT APPLICATION NUMBER: US/11/083,784	CURRENT FILING DATE: 2005-03-18					
	PRIOR APPLICATION NUMBER: US/10/714,333	PRIOR FILING DATE: 2003-11-14					
	PRIOR APPLICATION NUMBER: 60/502,050	PRIOR FILING DATE: 2003-09-10					
	PRIOR APPLICATION NUMBER: 60/426,137	PRIOR FILING DATE: 2002-11-14					
	NUMBER OF SEQ ID NOS: 1591911	SOFTWARE: Proprietary					
	SEQ ID NO 161190	LENGTH: 19					
	TYPE: RNA	ORGANISM: Homo sapiens					
	US-11-083-784-161190	Sequence 161190, Application US/11083784					
	Publication No. US20050245475A1	GENERAL INFORMATION:					
	APPLICANT: Dharmacon, Inc.	APPLICANT: Khvorova, Anastasia					
	APPLICANT: Reynolds, Angela	APPLICANT: Marshall, William					
	APPLICANT: Scaringe, Stephen	APPLICANT: Scaringe, Stephen					
	FILE REFERENCE: 13499US	TITLE OF INVENTION: Functional and Hyperfunctional siRNA					
	CURRENT APPLICATION NUMBER: US/11/083,784	CURRENT FILING DATE: 2005-03-18					
	PRIOR APPLICATION NUMBER: US/10/714,333	PRIOR FILING DATE: 2003-11-14					
	PRIOR APPLICATION NUMBER: 60/502,050	PRIOR FILING DATE: 2003-09-10					
	PRIOR APPLICATION NUMBER: 60/426,137	PRIOR FILING DATE: 2002-11-14					
	NUMBER OF SEQ ID NOS: 1591911	SOFTWARE: Proprietary					
	SEQ ID NO 161190	LENGTH: 19					
	TYPE: RNA	ORGANISM: Homo sapiens					
	US-11-083-784-161190	Sequence 161190, Application US/11083784					
	Publication No. US20050245475A1	GENERAL INFORMATION:					
	APPLICANT: Dharmacon, Inc.	APPLICANT: Khvorova, Anastasia					
	APPLICANT: Reynolds, Angela	APPLICANT: Marshall, William					
	APPLICANT: Scaringe, Stephen	APPLICANT: Scaringe, Stephen					
	FILE REFERENCE: 13499US	TITLE OF INVENTION: Functional and Hyperfunctional siRNA					
	CURRENT APPLICATION NUMBER: US/11/083,784	CURRENT FILING DATE: 2005-03-18					
	PRIOR APPLICATION NUMBER: US/10/714,333	PRIOR FILING DATE: 2003-11-14					
	PRIOR APPLICATION NUMBER: 60/502,050	PRIOR FILING DATE: 2003-09-10					
	PRIOR APPLICATION NUMBER: 60/426,137	PRIOR FILING DATE: 2002-11-14					
	NUMBER OF SEQ ID NOS: 1591911	SOFTWARE: Proprietary					
	SEQ ID NO 161190	LENGTH: 19					



```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 276299
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-276299

```

```

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 16 GGGGATCAACTCTGGA 32
    |||||:|:|:|:|
Db 2 GAGGAUACAGCUCUGGA 18

```

## RESULT 181

```

US-11-083-784-290226
; Sequence 290226, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 290226
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-290226

```

```

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 44 GGTAAGAGCCAGCGAA 60
    ||:|||||:|:|:|
Db 2 GGUAAGAGUCAGAGAA 18

```

## RESULT 182

```

US-11-083-784-290240
; Sequence 290240, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 290240
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-290240

```

```

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 44 GGTAAGAGCCAGCGAA 60
    ||:|||||:|:|:|
Db 1 GGUAAGAGUCAGAGAA 17

```

## RESULT 183

```

US-11-083-784-404405/c
; Sequence 404405, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 404405
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-404405

```

```

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 37 TCTGAGAGGTAAGAGC 53
    |||||:|:|:|:|
Db 17 TCTGAGGATAAGAGC 1

```

## RESULT 184

```

US-11-083-784-440203

```

```
; Sequence 440203, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 440203
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-440203

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AAACAAGACGCGCTGGG 18
Db      1 AAACAAGACGCGCGUGG 17

RESULT 185
US-11-083-784-524859
; Sequence 524859, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 524859
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-524859

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 1.5e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      21 TACAACCTCTGAGTCCT 37
Db      2 UACAACUCUGGAGUUGCU 18

RESULT 186
US-11-083-784-673690/c
; Sequence 673690, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 673690
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-673690

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CTGGGATACAACTCTG 30
Db      18 CTGAGGGTACAACTCTG 2

RESULT 187
US-11-083-784-681344
; Sequence 681344, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 681344
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-681344

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      23 CAACTCTGGAGTCCTCT 39
```



Query Match 17.9%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 35 CCTCTGAGAGGTAAGA 51  
| | | | | | | | | | | | | | | | | | | | |  
Db 18 CTTCGAGAGGTAACA 2

## RESULT 192

US-11-083-784-813171/c  
; Sequence 813171, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14,333  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 813171  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-813171

Query Match 17.9%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 21 TACACTCTCGAGTCCT 37  
| | | | | | | | | | | | | | | | | | | | |  
Db 19 TACAGCTCTCGAGTTCT 3

## RESULT 193

US-11-083-784-862664/c  
; Sequence 862664, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14,333  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 862664  
; LENGTH: 19

; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-862664

Query Match 17.9%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 ACTCTGAGTCCTCTGA 41  
| | | | | | | | | | | | | | | | | | | | |  
Db 17 ACACCGAGTCCTCTGA 1

## RESULT 194

US-11-083-784-900906  
; Sequence 900906, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14,333  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 900906  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-900906

Query Match 17.9%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 76.5%; Pred. No. 1.5e+02;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 38 CTGAGAGGTAAGAGCC 54  
| : | | | | | : | | | | | | | | | | | | | | |  
Db 2 CUGAGAGCUAAGAGAC 18

## RESULT 195

US-11-083-784-941347/c  
; Sequence 941347, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14,333  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911



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; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1069062
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1069062

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      46 TAAAGAGCCGCGAAGC 62
      ||||| ||||| |||||
Db      19 TAAATGCCAGCGAAGC 3

RESULT 200
US-11-083-784-1149570
; Sequence 1149570, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1149570
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1149570

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      60 AGCTGATGCTCTGCA 76
      ||||| ||||| |||||
Db      2 AGAUGAUGUCCUGCA 18

RESULT 201
US-11-083-784-1271626
; Sequence 1271626, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1271626
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1271626

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      58 GAAGCTGATGCTCTGTC 74
      ||||| ||||| |||||
Db      18 GAAGATGAAGTCCTGTC 2

RESULT 203
US-11-083-784-1286517/c
; Sequence 1286517, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286508
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1286508

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      58 GAAGCTGATGCTCTGTC 74
      ||||| ||||| |||||
Db      18 GAAGATGAAGTCCTGTC 2
```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286517
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1286517

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Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 58 GAAGCTGATGCTCGTC 74
    ||||| ||||| |||||
Db 19 GAAGATGAAGTCTCGTC 3

```

```

RESULT 204
US-11-083-784-1299503/c
; Sequence 1299503, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1299503
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1299503

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Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 55 AGCGAAGCTGATGTCCT 71
    ||||| ||||| |||||
Db 18 AGCAAGAGCTGATGACCT 2

```

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RESULT 205
US-11-083-784-1321159
; Sequence 1321159, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia

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; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1321159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1321159

```

```

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 18 GGATACAACTCTCGAGT 34
    ||||| ||||| |||||
Db 1 GGAUACAGCACUGGAGU 17

```

```

RESULT 206
US-11-083-784-1334132
; Sequence 1334132, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1334132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1334132

```

```

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 35 CCTCTGAGAGGTAAGA 51
    ||||| ||||| |||||
Db 1 CCUCUGAGAGUCACAGA 17

```

```

RESULT 207
US-11-083-784-1359524
; Sequence 1359524, Application US/11083784
; Publication No. US20050245475A1

```

```
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359524
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1359524

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCGCGAA 60
Db 1 GAUAAAGAGUCAGCGAA 17

RESULT 208
US-11-083-784-1359621
; Sequence 1359621, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359621
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1359621

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCGCGAA 60
Db 1 GAUAAAGAGUCAGCGAA 17

RESULT 209
US-11-083-784-1359621
; Sequence 1359621, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359621
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1359621

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCGCGAA 60
Db 1 GAUAAAGAGUCAGCGAA 17

RESULT 209
US-11-083-784-1510975
; Sequence 1510975, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1510975
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1510975

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 45 GTTAAAGAGCCGCGAAG 61
Db 1 GUGAAGAGCCAGTGAAG 17

RESULT 210
US-11-083-784-1510975
; Sequence 1510975, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1510975
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1510975

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 45 GTTAAAGAGCCGCGAAG 61
Db 1 GUGAAGAGCCAGTGAAG 17
```



## RESULT 211

US-11-083-784-1565567/c  
 ; Sequence 1565567, Application US/11083784  
 ; Publication No. US20050245475A1

## GENERAL INFORMATION:

; APPLICANT: Dharmoon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784

; CURRENT FILING DATE: 2005-03-18

; PRIOR APPLICATION NUMBER: US/10/714,333

; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 1565567

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-083-784-1565567

Query Match 17.9%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 1.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 47 AAAGAGCGCAGCGAGCT 63

Db 18 AATGAGCGCAGCGAGAT 2

## RESULT 212

US-10-310-914A-730939

; Sequence 730939, Application US/10310914A

; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvazat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 730939

; LENGTH: 18

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-730939

Query Match 17.4%; Score 13.4; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. No. 1.7e+02;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACAAGACGGCGCTGGG 18

Db 3 ACAAGACGGCGCUGUG 17

## RESULT 213

US-10-310-914A-819956

; Sequence 819956, Application US/10310914A

; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvazat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 819956

; LENGTH: 18

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-819956

Query Match 17.4%; Score 13.4; DB 1; Length 18;

Best Local Similarity 73.3%; Pred. No. 1.7e+02;

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 31 GAGTCCTCTCAGAGG 45

Db 1 GAGGCTCUCAGAGG 15

## RESULT 214

US-10-310-914A-1127926

; Sequence 1127926, Application US/10310914A

; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvazat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1127926

; LENGTH: 18

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1127926

Query Match 17.4%; Score 13.4; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. No. 1.7e+02;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACAAGACGGCGCTGGG 18

Db 3 ACAAGACGGCGCUGUG 17

## RESULT 215

US-10-310-914A-715225

; Sequence 715225, Application US/10310914A

; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvazat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 715225

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-715225

```
Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAACAAGACGGCGCTG 16
   |||||
Db 1 AAACAAGACGGCGUUG 15
   |||||

RESULT 216
US-10-310-914A-751334
; Sequence 751334, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 751334
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-751334

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 22 ACAACTCTGAGTCC 36
   ||| |:|:|:|
Db 5 ACACCCUGGAGUCC 19
   ||| |:|:|:|

RESULT 217
US-10-310-914A-1053707
; Sequence 1053707, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1053707
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1053707

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 42 GAGTAAAGACGCCAG 56
   |||||
Db 3 GAGGAAACAGCCAG 17
   |||||

RESULT 218
US-10-310-914A-1058236
; Sequence 1058236, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1058236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1058236
```

Query Match 17.4%; Score 13.4; DB 1; Length 19;

Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 31 GAGTCCTCTGAGGAGG 45

|||:|:|:|

Db 3 GAGUCCUCAGAGAGG 17

RESULT 219

```
US-10-310-914A-1241072
; Sequence 1241072, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
```

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1241072

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1241072

Query Match 17.4%; Score 13.4; DB 1; Length 19;

Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAACAAGACGGCGCT 15

|||||

Db 4 CAAACAACACGGCCU 18

RESULT 220

```
US-10-310-914A-1268592/c
; Sequence 1268592, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
```

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1268592

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1268592

```
Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 44 GGTAAAGAGCCAGCG 58
Db 18 GGTAAAGAGAGCAGCG 4

RESULT 221
US-10-310-914A-1370512/c
; Sequence 1370512, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shilet, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1370512
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1370512

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 22 ACAACTCTGGAGTCC 36
Db 17 AAAACTCTGGAGTCC 3

RESULT 222
US-11-101-244-24060/c
; Sequence 24060, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 24060
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-24060

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAAGAGC 53
Db 15 TGAGAGGCAAGAGC 1

RESULT 223
US-11-101-244-24159/c
; Sequence 24159, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 24159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-24159

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAAGAGC 53
Db 15 TGAGAGGCAAGAGC 1

RESULT 224
US-11-101-244-34612/c
; Sequence 34612, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 34612
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-34612

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 54 CAGCGAAGCTGATGT 68
Db 16 CAGTGAAGCTGATGT 2
```

```
RESULT 225
US-11-101-244-88668
; Sequence 88668, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 88668
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-88668

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      57 CGAAGCTGATGTCCT 71
Db      4 CGAAGCUUAGUCCU 18
|||||:|:|:|

RESULT 226
US-11-101-244-199690
; Sequence 199690, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 199690
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-199690

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CAAACAGACGGCCT 15
Db      1 CAAACAGACGGCCU 15
|||||:|:|:|

RESULT 227
US-11-101-244-387184
; Sequence 387184, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387184
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-387184

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      18 GGATCAACTCTGGA 32
Db      1 GGAUACAGCUCUGGA 15
|||||:|:|:|

RESULT 228
US-11-101-244-276236
; Sequence 276236, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 276236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-276236

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CAAACAGACGGCCT 15
Db      1 CAAACAGACGGCCU 15
|||||:|:|:|

RESULT 229
US-11-101-244-387184
; Sequence 387184, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387184
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-387184

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CAAACAGACGGCCT 15
Db      1 CAAACAGACGGCCU 15
|||||:|:|:|
```

; Sequence 387184, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 387184  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-387184

Query Match 17.4%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 86.7%; Pred. No. 1.6e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 46 TAAAGAGCCGCGAA 60  
Db 2 UAAAGAGCCGCGAA 16

RESULT 230  
US-11-101-244-387289  
; Sequence 387289, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 387289  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-387289

Query Match 17.4%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 86.7%; Pred. No. 1.6e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 46 TAAAGAGCCGCGAA 60  
Db 2 UAAAGAGCCGCGAA 16

RESULT 231  
US-11-101-244-387392  
; Sequence 387392, Application US/11101244

; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 387392  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-387392

Query Match 17.4%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 86.7%; Pred. No. 1.6e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 46 TAAAGAGCCGCGAA 60  
Db 2 UAAAGAGCCGCGAA 16

RESULT 232  
US-11-101-244-387492  
; Sequence 387492, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 387492  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-387492

Query Match 17.4%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 86.7%; Pred. No. 1.6e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 46 TAAAGAGCCGCGAA 60  
Db 2 UAAAGAGCCGCGAA 16

RESULT 233  
US-11-101-244-410730/C  
; Sequence 410730, Application US/11101244  
; Publication No. US20050246794A1

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 410730
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-410730

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 31 GAGTCCTCTGAGAGG 45
Db 18 GAGTCCTCTGAGATG 4

```

```

RESULT 234
US-11-101-244-410929/c
; Sequence 410929, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 410929
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-410929

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 31 GAGTCCTCTGAGAGG 45
Db 18 GAGTCCTCTGAGATG 4

```

```

RESULT 235
US-11-101-244-411027/c
; Sequence 411027, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 411027
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-411027

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 31 GAGTCCTCTGAGAGG 45
Db 18 GAGTCCTCTGAGATG 4

```

```

RESULT 236
US-11-101-244-512370/c
; Sequence 512370, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 512370
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-512370

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 22 ACAACACTGAGATGCC 36
Db 15 ACAACACTGAGATGCC 1

```

```

RESULT 237
US-11-101-244-527876/c
; Sequence 527876, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.

```

; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 527876  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-527876

Query Match 17.4%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCTGT 73  
||| ||||| ||||| |||||  
Db 19 AATCTGATGTCCTGT 5

RESULT 238  
US-11-101-244-539325  
; Sequence 539325, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 539325  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-539325

Query Match 17.4%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 60.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 63 TGATGTCCTGTCAAG 77  
: ||| ||| ||| |||  
Db 3 UCAUGUCCUGUCAAG 17

RESULT 239  
US-11-101-244-550822  
; Sequence 550822, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 550822  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-550822

Query Match 17.4%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 73.3%; Pred. No. 1.6e+02;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 30 GGAGTCTCTGAGAG 44  
||| ||| ||| |||  
Db 1 GGAGUCCUCUGGAG 15

RESULT 240  
US-11-101-244-550923  
; Sequence 550923, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 550923  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-550923

Query Match 17.4%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 73.3%; Pred. No. 1.6e+02;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 30 GGAGTCTCTGAGAG 44  
||| ||| ||| |||  
Db 1 GGAGUCCUCUGGAG 15

RESULT 241  
US-11-101-244-581627  
; Sequence 581627, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 581627
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-581627

```

```

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 37 TCTGAGAGGTAAAGA 51
   |:|||||:|
Db 1 UCUCAGAGGUAAAGA 15

```

```

RESULT 242
US-11-101-244-624448
; Sequence 624448, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 624448
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-624448

```

```

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 58 GAAGCTGATGCTCTG 72
   |||||:|:|
Db 5 GAAGCUGAUGUCAUG 19

```

```

RESULT 243
US-11-101-244-680973
; Sequence 680973, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 680973
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-680973

```

```

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 59 AGCTGATGCTCTGT 73
   |||||:|:|
Db 3 AGGCUGAUGCCUGU 17

```

```

RESULT 244
US-11-101-244-686033
; Sequence 686033, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 686033
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-686033

```

```

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 18 GGATACAACTCTGGA 32
   |||||:|:|
Db 1 GGAUACACACUCUGA 15

```

```

RESULT 245
US-11-101-244-710507
; Sequence 710507, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```



```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 710507
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-710507

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      47 AAAGAGCCGAGGAG 61
        |||||
DB      3 AAAGAGCCGAGGAG 17

```

```

RESULT 246
US-11-101-244-710553
; Sequence 710553, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 710553
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-710553

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      47 AAAGAGCCGAGGAG 61
        |||||
DB      5 AAAGAGCCGAGGAG 19

```

```

RESULT 247
US-11-101-244-785114
; Sequence 785114, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 785114
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-785114

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      46 TAAAGAGCCGAGGAA 60
        :|||
DB      1 UAAAGAGCCGAGGAA 15

```

```

RESULT 248
US-11-101-244-785140
; Sequence 785140, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 785140
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-785140

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      46 TAAAGAGCCGAGGAA 60
        :|||
DB      2 UAAAGAGCCGAGGAA 16

```

```

RESULT 249
US-11-101-244-795267
; Sequence 795267, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

```

```
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 795267
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-795267

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 63 TGATGTCCTGTCAG 77
Db 5 UGAUCCUGGUCGCAAG 19

RESULT 250
US-11-101-244-833429
; Sequence 833429, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 833429
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-833429

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGCTCT 71
Db 4 CAAAGCUGGUGGUCU 18

RESULT 251
US-11-101-244-878459
; Sequence 878459, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 878459
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-878459

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCAGCGAA 60
Db 19 TAAAGAGCCAGTGAA 5

RESULT 253
US-11-101-244-972474/c
; Sequence 972474, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 972375
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-972375

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCAGCGAA 60
Db 19 TAAAGAGCCAGTGAA 5
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; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 972474
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-972474

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      46 TAAAGAGCCGCGAA 60
Db      19 TAAAGAGCCAGTGAA 5

RESULT 254
US-11-101-244-101248
; Sequence 101248, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 101248
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-101248

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      58 GAAGCTGATGCTCTG 72
Db      2 GAAGAUGAGUCCUG 16

RESULT 255
US-11-101-244-1034219/c
; Sequence 1034219, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1034219
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1034219

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      60 AGCTGATGCTCTGTC 74
Db      15 AGCTGAGTCTCTGTC 1

RESULT 256
US-11-101-244-1036393
; Sequence 1036393, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1036393
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1036393

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      47 AAAGAGCCGCGAAG 61
Db      2 AAAGAGCCGCGAAG 16

RESULT 257
US-11-101-244-1155168
; Sequence 1155168, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050

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; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1249609
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1249609

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 23 CAACCTGGAGTCCT 37
Db 1 CAACUCUGGUGUCU 15

RESULT 258
US-11-101-244-1235172/c
; Sequence 1235172, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1235172
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1235172

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AACAGAGCGCCTGG 17
Db 19 AACAGACTGCCTGG 5

RESULT 259
US-11-101-244-1249609/c
; Sequence 1249609, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1249609
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1249609

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 CTCGAGGTCTCTCTG 40
Db 18 CTCGGAGGCCCTCTG 4

RESULT 261
US-11-101-244-1327400/c
; Sequence 1327400, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1326829
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1326829

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 CTCGAGGTCTCTCTG 40
Db 18 CTCGGAGGCCCTCTG 4

RESULT 260
US-11-101-244-1326829/c
; Sequence 1326829, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1326829
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1326829

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCTCTG 72
Db 15 GAAGCTGTGTCTCTG 1
```

```
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1327400
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1327400

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGTCCTG 72
Db 18 GAAGCTGAGGTCCTG 4

RESULT 262
US-11-101-244-1327433/c
; Sequence 1327433, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1327433
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1327433

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGTCCTG 72
Db 16 GAAGCTGAGGTCCTG 2

RESULT 263
US-11-101-244-1351972/c
; Sequence 1351972, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1327433
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1351972

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGTCCTG 72
Db 16 GAAGCTGAGGTCCTG 2

RESULT 264
US-11-101-244-1359582
; Sequence 1359582, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359582
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1359582

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TAAAGAGCCGCGAA 60
Db 2 UAAAGAGUCAGCGAA 16

RESULT 265
US-11-101-244-1359676
; Sequence 1359676, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359676
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1359676

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TAAAGAGCCGCGAA 60
Db 2 UAAAGAGUCAGCGAA 16
```

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; SOFTWARE: Proprietary
; SEQ ID NO 1359676
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1359676

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGACGAA 60
Db 2 UAAAGAGCUGACGAA 16

RESULT 266
US-11-101-244-1418701
; Sequence 1418701, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1418701
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1418701

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 54 CAGCGAGCTGATGT 68
Db 1 CAGGAGCUGAUGU 15

RESULT 267
US-11-101-244-1435574/c
; Sequence 1435574, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1435574
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1435574

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGA 41
Db 15 TCTGGAGACCTCTGA 1

RESULT 268
US-11-101-244-1492356/c
; Sequence 1492356, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1492356
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1492356

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGA 41
Db 17 TCTGGTGTCTCTGA 3

RESULT 269
US-11-101-244-1512594/c
; Sequence 1512594, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1512594
```

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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1512594

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGA 32
Db 16 GGATACAACTCTGAA 2

RESULT 270
US-11-101-244-1522587
; Sequence 1522587, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1522587
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1522587

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 38 CTGAGAGGTTAAAGAG 52
Db 2 CUCAGAGGUAAGAG 16

RESULT 271
US-11-101-244-1560555
; Sequence 1560555, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1560555
; LENGTH: 19
; TYPE: RNA
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1560555

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAACAGACGGCCT 15
Db 1 CAAACAGAGGGCCU 15

RESULT 272
US-11-101-244-1570062
; Sequence 1570062, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1570062
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1570062

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCGCGAAG 61
Db 2 AAAGAGCCGCGAAG 16

RESULT 273
US-11-101-244-1570074
; Sequence 1570074, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1570074
; LENGTH: 19
; TYPE: RNA
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-24060

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAG 61
    |||||
Db 3 AAAGAGCCAGCGAAG 17

RESULT 274
US-11-083-784-24060/c
; Sequence 24060, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1590808
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-24060/c

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTG 72
    |||||
Db 2 GAAGCAGAUGUCCUG 16

RESULT 275
US-11-083-784-24060/c
; Sequence 24060, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 24060
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-24060/c

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAAGAGC 53
    |||||
Db 15 TGAGAGGCAAGAGC 1

RESULT 276
US-11-083-784-24159/c
; Sequence 24159, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 24159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-24159/c

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAAGAGC 53
    |||||
Db 15 TGAGAGGCAAGAGC 1

RESULT 277
US-11-083-784-34612/c
; Sequence 34612, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 34612
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-34612/c
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; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 276236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-276236

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGA 32
   |||:|||||:||||
Db 1 GGAUACAGCTCUGGA 15

RESULT 282
US-11-083-784-387184
; Sequence 387184, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387184
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387184

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGCGAA 60
   :|||||||:|||||
Db 2 UAAAGAGCCGCGAA 16

RESULT 284
US-11-083-784-387392
; Sequence 387392, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387392
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387392

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGCGAA 60
   :|||||||:|||||
Db 2 UAAAGAGCCGCGAA 16

RESULT 285
US-11-083-784-387492
; Sequence 387492, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
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; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387492
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387492

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      46 TAAAGAGCCGACGAA 60
Db      2 UAAAGAGCCUGCGAA 16

RESULT 286
US-11-083-784-410730/c
; Sequence 410730, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 410730
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-410730

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      31 GAGTCCTCTGAGAGG 45
Db      18 GAGTCCTCTGAGATG 4

RESULT 287
US-11-083-784-410929/c
; Sequence 410929, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 410730
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-410730

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      31 GAGTCCTCTGAGAGG 45
Db      18 GAGTCCTCTGAGATG 4

RESULT 288
US-11-083-784-411027/c
; Sequence 411027, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 411027
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-411027

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      31 GAGTCCTCTGAGAGG 45
Db      18 GAGTCCTCTGAGATG 4

RESULT 289
US-11-083-784-512370/c
; Sequence 512370, Application US/11083784
; Publication No. US20050245475A1
; APPLICANT: Khvorova, Anastasia
```

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; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 512370
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-512370

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      22  ACAACTCTGGAGTCC 36
Db      15  ACAACACTGGAGTCC 1

RESULT 290
US-11-083-784-527876/c
; Sequence 527876, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 527876
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-527876

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      59  AACCTGATGCTCTGT 73
Db      19  AATCTGATGCTCTGT 5

RESULT 291
US-11-083-784-527876/c
; Sequence 527876, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 527876
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-527876

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      59  AACCTGATGCTCTGT 73
Db      19  AATCTGATGCTCTGT 5

US-11-083-784-539325
; Sequence 539325, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 539325
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-539325

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      63  TGATGCTCTGTCAAG 77
Db      3   UCAUGUCCUGUCAAG 17

RESULT 292
US-11-083-784-550822
; Sequence 550822, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 550822
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-550822

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      30  GGAGTCTCTGTGAG 44
Db      1   GGAGUCCUCUGGAG 15
```



```
Best Local Similarity 60.0%; Pred. No. 1.6e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 5;

QY 59 AGCTGATGTCCTGT 73
| |:| |:| |:| |:|
Db 3 AGCGAUGGUCCUGU 17

RESULT 297
US-11-083-784-686033
; Sequence 686033, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 686033
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-686033

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGA 32
| |:| |:| |:| |:|
Db 1 GGAUACAACACUGA 15

RESULT 298
US-11-083-784-710507
; Sequence 710507, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 710507
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-710507

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAG 61
| |:| |:| |:| |:|
Db 5 AAAGAGCCAGCGAAG 19

RESULT 299
US-11-083-784-710553
; Sequence 710553, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 710553
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-710553

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAG 61
| |:| |:| |:| |:|
Db 5 AAAGAGCCAGCGAAG 19

RESULT 300
US-11-083-784-785114
; Sequence 785114, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 785114
```

```
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-785114

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TAAAGAGCCGCGAA 60
   :|||||
Db 1 UAAAGAGCGCGAA 15

RESULT 301
US-11-083-784-785140
; Sequence 785140, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 785140
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-785140

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TAAAGAGCCGCGAA 60
   :|||||
Db 2 UAAAGAGCGCGAA 16

RESULT 302
US-11-083-784-795267
; Sequence 795267, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 785140
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-785140

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TAAAGAGCCGCGAA 60
   :|||||
Db 2 UAAAGAGCGCGAA 16

RESULT 303
US-11-083-784-833429
; Sequence 833429, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 833429
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-833429

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGCTCT 71
   :|||||
Db 4 CAAAGCGAUGUCCU 18

RESULT 304
US-11-083-784-878459
; Sequence 878459, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
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; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 878459
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-878459

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 60 AGCTGATGTCCTCTC 74
Db 2 AGCUGGUGCCUGUC 16

RESULT 305
US-11-083-784-972375/c
; Sequence 972375, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 972375
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-972375

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCAGCGAA 60
Db 19 TAAAGAGCCAGTGAA 5

RESULT 306
US-11-083-784-972474/c
; Sequence 972474, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18

; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 878459
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-878459

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 60 AGCTGATGTCCTCTC 74
Db 2 AGCUGGUGCCUGUC 16

RESULT 307
US-11-083-784-1012488
; Sequence 1012488, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1012488
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1012488

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTG 72
Db 2 GAAGAUGAUGCCUG 16

RESULT 308
US-11-083-784-1034219/c
; Sequence 1034219, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
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```
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1249609
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1249609

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTG 72
Db 15 GAAGCTGTTGTCCTG 1

RESULT 313
US-11-083-784-1326829/c
; Sequence 1326829, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1326829
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1326829

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 CTCCTGGAGTCCTCG 40
Db 18 CTCCTGGAGGCTCTG 4

RESULT 314
US-11-083-784-1327400/c
; Sequence 1327400, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1327400
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1327400

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTG 72
Db 16 GAAGCTGAGGTCCTG 2

RESULT 315
US-11-083-784-1327433/c
; Sequence 1327433, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1327433
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1327433

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTG 72
Db 16 GAAGCTGAGGTCCTG 2
```

```

RESULT 316
US-11-083-784-1351972/c
; Sequence 1351972, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1351972
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1351972

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      18 GGATACAACTCTGGA 32
      ||| ||||| ||||| |||
Db      17 GGAGACAACTCTGGA 3

RESULT 317
US-11-083-784-1359582
; Sequence 1359582, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359582
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1359582

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      46 TAAAGAGCGCGGAA 60
      :||||| ||||| |||||
Db      2 UAAAGAGCGCGGAA 16

RESULT 318
US-11-083-784-1359676
; Sequence 1359676, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359676
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1359676

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      46 TAAAGAGCGCGGAA 60
      :||||| ||||| |||||
Db      2 UAAAGAGCGCGGAA 16

RESULT 319
US-11-083-784-1418701
; Sequence 1418701, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1418701
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1418701

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 54 CAGCGAAGCTGTGT 68
    ||| ||| ||| ||| |||
Db 1 CAGUGAAGCUGAUGU 15

RESULT 320
US-11-083-784-1435574/c
; Sequence 1435574, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1435574
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1435574

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGA 41
    ||| ||| ||| ||| |||
Db 15 TCTGGAGACCTCTGA 1

RESULT 321
US-11-083-784-1492356/c
; Sequence 1492356, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1492356
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1492356

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGA 41
    ||| ||| ||| ||| |||
Db 15 TCTGGAGACCTCTGA 1

RESULT 322
US-11-083-784-1512594/c
; Sequence 1512594, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1512594
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1512594

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGA 32
    ||| ||| ||| ||| |||
Db 16 GGATACAACTCTGAA 2

RESULT 323
US-11-083-784-1522587
; Sequence 1522587, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1522587
; LENGTH: 19
; TYPE: RNA
US-11-083-784-1522587

```

```
; ORGANISM: Homo sapiens
US-11-083-784-1522587

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 38 CTGAGAGGTAAAG 52
   |:|||||:|||||
Db 2 CUCAGAGGUAAGAG 16

RESULT 324
US-11-083-784-1560555
; Sequence 1560555, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1560555
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1560555

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAACAGAGCGGCT 15
   |||||||:|||||
Db 1 CAAACAGAGUGGCU 15

RESULT 325
US-11-083-784-1570062
; Sequence 1570062, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
US-11-083-784-1570062
```

```
; SEQ ID NO 1570062
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1570062

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCGCGAAG 61
   |||||||:|||||
Db 2 AAAGAGCCGCGAAG 16

RESULT 326
US-11-083-784-1570074
; Sequence 1570074, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1570074
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1570074

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCGCGAAG 61
   |||||||:|||||
Db 3 AAAGAGCCGCGAAG 17

RESULT 327
US-11-083-784-1590808
; Sequence 1590808, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
US-11-083-784-1590808
```

; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1590808  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1590808

Query Match 17.4%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 73.3%; Pred. No. 1.8e+02;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATCTCTG 72  
||||| |||:|:  
Db 2 GAAGCAGAUCCUG 16

RESULT 328  
US-10-310-914A-128513/c  
; Sequence 128513, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087, 0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 128513  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-128513

Query Match 17.1%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 40 GAGAGGTAAGAGCCAGC 57  
||||| |||:|:  
Db 18 GAGAGGGAGAGCGAGC 1

RESULT 329  
US-10-310-914A-176877  
; Sequence 176877, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087, 0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 176877  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-176877

Query Match 17.1%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.8e+02;  
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 35 CCTCTGAGGTAAGAG 52  
||:|:|||| |

Db 1 CCUCUGAGAGUAGGAG 18

RESULT 330  
US-10-310-914A-721777  
; Sequence 721777, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087, 0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 721777  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-721777

Query Match 17.1%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 AGAGGTAAGAGCCAGCG 58  
||||| |||:|:  
Db 1 AGAGGAAGAGAGGAGCG 18

RESULT 331  
US-10-310-914A-794232  
; Sequence 794232, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087, 0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 794232  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-794232

Query Match 17.1%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 28 CTGGACTCCTCTGAGAGG 45  
||||| |||:|:  
Db 1 CAGGAGUCCUCUAGGAGG 18

RESULT 332  
US-10-310-914A-956449  
; Sequence 956449, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087, 0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 956449  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-956449

Query Match 17.1%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 77.8%; Pred. No. 1.8e+02;  
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 AAACAAGAGCGCTGGGG 19  
Db 1 AGACAGGAGGCCUGGG 18

## RESULT 333

US-10-310-914A-970022/c  
; Sequence 970022, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 970022  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-970022

Query Match 17.1%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 38 CTGAGAGGTAAGAGCCA 55  
Db 18 CTGAGAGCTTAAGAGCTA 1

## RESULT 334

US-10-310-914A-1268240/c  
; Sequence 1268240, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1268240  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1268240

Query Match 17.1%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 25 ACTCTGAGTCCTCTGAG 42  
Db 18 ACTCTGAATCCTATGG 1

## RESULT 335

US-10-310-914A-1213531  
; Sequence 1213531, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1213531  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1213531

Query Match 16.9%; Score 13; DB 1; Length 18;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Qy 26 CTCTGAGTCCTC 38  
Db 6 CUCUGAGGUCC 18

## RESULT 336

US-10-750-185-15896/c  
; Sequence 15896, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15896  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Forward Primer  
US-10-750-185-15896

Query Match 16.6%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 42 GAGGTAAAGAGCCAGC 57  
Db 16 GAGGTAGAGCCAGC 1

## RESULT 337

US-10-750-623-15896/c  
; Sequence 15896, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:

```
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: FANTIN, Dennis
/ APPLICANT: BATES, Stephen
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: WM1100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 15896
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Forward Primer
US-10-750-623-15896

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 42 GAGCTAAGGCCAGC 57
   ||||| |||||
Db 16 GAGGTTAGGCCAGC 1

RESULT 338
US-10-310-914A-198185
/ Sequence 198185, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiler, Kvuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 198185
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-198185

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCCTGGGATACAACT 27
   ||| |||||:||||:
Db 3 GCCAGGAUAACAACU 18

RESULT 339
US-10-310-914A-319191
/ Sequence 319191, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiler, Kvuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
```

```
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 319191
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-319191

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 37 TCTGAGAGGTAAGAG 52
   :|||:|||||
Db 3 UCUGAGAGGCACAGAG 18

RESULT 340
US-10-310-914A-537246/c
/ Sequence 537246, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiler, Kvuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 537246
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-537246

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGTC 74
   ||||| |||||
Db 17 AAGCTGATTCCTGCC 2

RESULT 341
US-10-310-914A-560230/c
/ Sequence 560230, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiler, Kvuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 560230
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-560230

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCCTTGAGAG 44
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Db 16 TGGAGGCTCTGGGAG 1
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RESULT 342
US-10-310-914A-575025
; Sequence 575025, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 575025
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-575025

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      34 TCCTCTGAGAGGTAAG 49
      :||:|: ||| |||
Db      1 UCCUCUAGAAGUAA 16

RESULT 343
US-10-310-914A-586396/c
; Sequence 586396, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 586396
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-586396

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      34 TCCTCTGAGAGGTAAG 49
      :||:|: ||| |||
Db      1 UCCUCUAGAAGUAA 16

RESULT 344
US-10-310-914A-784421
; Sequence 784421, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 784421
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-784421

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      50 GAGCCAGCGAAGCTGA 65
      ||||| ||||| |||
Db      17 GAGCCGCGAAGCGGA 2

RESULT 345
US-10-310-914A-815477
; Sequence 815477, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 815477
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-815477

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 2e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      35 CCTCTGAGAGGTAAG 50
      ||:|: ||||| ||||
Db      3 CCUCAGAGGCAAG 18

RESULT 346
US-10-310-914A-919520/c
; Sequence 919520, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 919520
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-919520

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      43 AGGTAAGAGCCAGCG 58
      ||||| ||||| |||
Db      18 AGGTGAAGAGCCAGCG 3
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 784421
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-784421

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 2e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      49 AGAGCCAGCGAAGCTG 64
      ||||| ||||| |||
Db      3 AGAGGGAGCGAAGCUG 18

RESULT 345
US-10-310-914A-815477
; Sequence 815477, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 815477
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-815477

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 2e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      35 CCTCTGAGAGGTAAG 50
      ||:|: ||||| ||||
Db      3 CCUCAGAGGCAAG 18

RESULT 346
US-10-310-914A-919520/c
; Sequence 919520, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 919520
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-919520

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      43 AGGTAAGAGCCAGCG 58
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Db      18 AGGTGAAGAGCCAGCG 3
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RESULT 347
US-10-310-914A-1087593
; Sequence 1087593, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1087593
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1087593

Query Match          16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 15 TGGGGATACAACTCTG 30
Db 1 UGGGGCUACACCUUG 16

RESULT 348
US-10-310-914A-1209729/c
; Sequence 1209729, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1209729
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1209729

Query Match          16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 61 GCTGATGTCCTGTCAC 76
Db 16 GCTGATGTCCTGACCA 1

RESULT 349
US-10-310-914A-1353151
; Sequence 1353151, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 1353151
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1353151

Query Match          16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 2e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAAGCTGA 65
Db 2 GAGACAGCGAAGCTCA 17

RESULT 350
US-10-310-914A-1354913
; Sequence 1354913, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1354913
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1354913

Query Match          16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 47 AAAGCCAGCGAAGC 62
Db 3 AAAGACAGCAGAGAAGC 18

RESULT 351
US-10-505-263-37/c
; Sequence 37, Application US/10505263
; Publication No. US20060014940A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Case Western Reserve University
; APPLICANT: The Brigham and Women's Hospital, Inc.
; APPLICANT: Mount, David B
; APPLICANT: Romero, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2
; FILE REFERENCE: 1242/50/2 PCT/US
; CURRENT APPLICATION NUMBER: US/10/505,263
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 60/360,275
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US03/06469
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-505-263-37

Query Match          15.6%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GACGGCCTGGGG 19

Db 12 GACGGCCTGGGG 1

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Job time : 1 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocorelation Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: April 19, 2006, 16:06:39 ; Search time 0.001 Seconds  
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403.480 Million cell updates/sec  
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Perfect score: 77  
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Gapop 10.0 , Gapext 0.5  
Searched: 181 seqs, 2620 residues  
Total number of hits satisfying chosen parameters: 362  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 182 summaries  
Database : gedsb:\*

GenBank/EMBL

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
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C 2	28.2	36.6	33 1	ACCESSION:I23840
C 3	21	27.3	21 1	ACCESSION:AR074251
C 4	21	27.3	21 1	ACCESSION:AX032613
C 5	15.4	20.0	22 1	BD185713
C 6	14.8	19.2	20 1	BD089289
C 7	14.8	19.2	21 1	ACCESSION:AR228291
C 8	14.4	18.7	17 1	ACCESSION:CO625286
C 9	14.4	18.7	17 1	ACCESSION:CO625287
C 10	14.4	18.7	17 1	ACCESSION:AR466349
C 11	14.4	18.7	17 1	ACCESSION:AR466350
C 12	14.4	18.7	17 1	ACCESSION:AR085604
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C 14	14.4	18.2	17 1	CO625285
C 15	14.4	18.2	17 1	AR466347
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C 21	13.4	17.4	17 1	AX649092
C 22	13.4	17.4	17 1	AX674032
C 23	13.4	17.4	17 1	AX732023
C 24	13.4	17.4	17 1	AX738057
C 25	13.4	17.4	17 1	AX738057
C 26	13.2	17.1	18 1	AR16421
C 27	13.2	17.1	18 1	AR16421
C 28	13.2	17.1	18 1	AR16424
C 29	13.2	17.1	18 1	I19537
C 30	13.2	17.1	18 1	I19540
C 31	13.2	17.1	18 1	I86217
C 32	13.2	17.1	18 1	I86220
C 33	13.2	17.1	18 1	AR584728
C 34	13.2	17.1	18 1	AX207952

C 34	13.2	17.1	18 1	AX473057
C 35	13	16.9	17 1	CO625283
C 36	13	16.9	17 1	AR466346
C 37	12.8	16.6	17 1	AX649089
C 38	12.8	16.6	17 1	AX762338
C 39	12.4	16.1	17 1	CO625289
C 40	12.4	16.1	17 1	AR286445
C 41	12.4	16.1	17 1	AR398435
C 42	12.4	16.1	17 1	AR466352
C 43	12.4	16.1	17 1	AX649087
C 44	12.4	16.1	17 1	AX649088
C 45	12.4	16.1	17 1	AX649093
C 46	12.4	16.1	17 1	AX734726
C 47	12.2	15.8	17 1	BD203204
C 48	12.2	15.8	17 1	AX687578
C 49	12.2	15.8	17 1	AX727379
C 50	12	15.6	16 1	CO858651
C 51	12	15.6	17 1	CO625282
C 52	12	15.6	17 1	AR466345
C 53	11.8	15.3	16 1	AR329584
C 54	11.8	15.3	16 1	AR362384
C 55	11.8	15.3	16 1	AR362385
C 56	11.4	14.8	16 1	AR029815
C 57	11.2	14.5	16 1	BD106403
C 58	11.2	14.5	16 1	I18626
C 59	11.2	14.5	16 1	AR305492
C 60	11.2	14.5	16 1	AR309596
C 61	11.2	14.5	16 1	AR455592
C 62	11.2	14.5	16 1	AR630011
C 63	11.2	14.5	16 1	AX351113
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C 76	10.8	14.0	15 1	BD207153
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C 78	10.8	14.0	15 1	CS004712
C 79	10.8	14.0	15 1	CS005312
C 80	10.8	14.0	15 1	I39319
C 81	10.8	14.0	15 1	I39320
C 82	10.8	14.0	15 1	I57649
C 83	10.8	14.0	15 1	I61819
C 84	10.8	14.0	15 1	AX635599
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C 102	10	13.0	10 1	BD248338
C 103	10	13.0	10 1	I22447
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C 105	10	13.0	10 1	I64511
C 106	10	13.0	10 1	AR238724

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107 10 13.0 10 1 AR270938 ACCESSION:AR270938
108 10 13.0 10 1 AX016299 ACCESSION:AX016299
109 10 13.0 10 1 AX152307 ACCESSION:AX152307
110 10 13.0 10 1 BD023238 ACCESSION:BD023238
111 10 13.0 13 1 AR641426 ACCESSION:AR641426
112 10 13.0 14 1 AR051174 ACCESSION:AR051174
113 10 13.0 14 1 BD068997 ACCESSION:BD068997
114 10 13.0 14 1 BD197865 ACCESSION:BD197865
115 10 13.0 14 1 I15960 ACCESSION:I15960
116 10 13.0 14 1 AR403497 ACCESSION:AR403497
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118 9.8 12.7 13 1 E15186 ACCESSION:E15186
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133 9.8 12.7 14 1 I78251 ACCESSION:I78251
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140 9.8 12.7 14 1 AR403429 ACCESSION:AR403429
141 9.8 12.7 14 1 AX467015 ACCESSION:AX467015
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143 9.8 12.7 14 1 BD000925 ACCESSION:BD000925
144 9.8 12.7 14 1 BD001354 ACCESSION:BD001354
145 9.8 12.7 14 1 S81872811 ACCESSION:S81872811
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149 9.4 12.2 11 1 CQ835946 ACCESSION:CQ835946
150 9.4 12.2 11 1 CQ836081 ACCESSION:CQ836081
151 9.4 12.2 11 1 CQ836100 ACCESSION:CQ836100
152 9.4 12.2 11 1 CQ837567 ACCESSION:CQ837567
153 9.4 12.2 11 1 CS021382 ACCESSION:CS021382
154 9.4 12.2 11 1 CS058360 ACCESSION:CS058360
155 9.4 12.2 11 1 CS058436 ACCESSION:CS058436
156 9.4 12.2 11 1 CS058451 ACCESSION:CS058451
157 9.4 12.2 11 1 CS058533 ACCESSION:CS058533
158 9.4 12.2 11 1 AX625866 ACCESSION:AX625866
159 9.4 12.2 11 1 AX627490 ACCESSION:AX627490
160 9.4 12.2 11 1 AX628152 ACCESSION:AX628152
161 9.4 12.2 11 1 AX630121 ACCESSION:AX630121
162 9.4 12.2 11 1 BD240909 ACCESSION:BD240909
163 9.4 12.2 12 1 CQ766172 ACCESSION:CQ766172
164 9.4 12.2 12 1 CQ766282 ACCESSION:CQ766282
165 9.4 12.2 12 1 CS104143 ACCESSION:CS104143
166 9.4 12.2 12 1 CS104143 ACCESSION:CS104143
167 9.4 12.2 12 1 AR475028 ACCESSION:AR475028
168 9.4 12.2 12 1 AX097978 ACCESSION:AX097978
169 9.4 12.2 12 1 AX138554 ACCESSION:AX138554
170 9.4 12.2 12 1 AX772212 ACCESSION:AX772212
171 9.4 12.2 13 1 AR019451 ACCESSION:AR019451
172 9.4 12.2 13 1 AR029150 ACCESSION:AR029150
173 9.4 12.2 13 1 AR036534 ACCESSION:AR036534
174 9.4 12.2 13 1 AR096067 ACCESSION:AR096067
175 9.4 12.2 13 1 AR156401 ACCESSION:AR156401
176 9.4 12.2 13 1 AR174824 ACCESSION:AR174824
177 9.4 12.2 13 1 CQ828552 ACCESSION:CQ828552
178 9.4 12.2 13 1 AR212300 ACCESSION:AR212300
179 9.4 12.2 13 1 AR285769 ACCESSION:AR285769

180 9.4 12.2 13 1 AR397760 ACCESSION:AR397760
181 9.4 12.2 13 1 AR658253 ACCESSION:AR658253
182 9.4 12.2 13 1 AX813993 ACCESSION:AX813993

ALIGNMENTS

RESULT 1
A23021/c 33 bp DNA linear PAT 06-DEC-1994
LOCUS 3' oligonucleotide.
DEFINITION A23021
ACCESSION A23021
VERSION A23021.1 GI:833241
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS EXPRESSION SYSTEMS
TITLE Patent: WO 92/11380-A 3 09-JUL-1992;
JOURNAL Location/Qualifiers
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QY 8 GACGGCTGGGATACAACTCTGGAGTCCTCTG 40
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RESULT 2
I23840/c 33 bp DNA linear PAT 07-OCT-1996
LOCUS Sequence 4 from patent US 553885.
DEFINITION I23840
ACCESSION I23840
VERSION I23840.1 GI:1603710
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Hollis,M., Needham,M.R.C., Gooding,C., Grosveld,F.G. and
Antoniou,M.
TITLE Expression systems
JOURNAL Patent: US 553885-A 4 23-JUL-1996;
FEATURES Location/Qualifiers
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Query Match 36.6%; Score 28.2; DB 1; Length 33;
Best Local Similarity 90.9%; Pred. No. 0.1;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 GACGGCTGGGATACAACTCTGGAGTCCTCTG 40
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DB 33 GACGGCTGGGATACAACTCTGGAGTCCTG 1

RESULT 3
AR074251/c 21 bp DNA linear PAT 28-AUG-2000
LOCUS AR074251
DEFINITION Sequence 59 from patent US 5952490.
ACCESSION AR074251
VERSION AR074251.1 GI:10001006
KEYWORDS
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SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y., Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and Imbach,J.Louis.  
 TITLE Oligonucleotides having a conserved G4 core sequence  
 JOURNAL Patent: US 5952490-A 59 14-SEP-1999;  
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 /mol\_type="unassigned DNA"  
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 Db 21 ATCAACTCTGGAGTCCTCTG 1  
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 AX032613/c  
 LOCUS AX032613 21 bp DNA linear PAT 20-SEP-2000  
 DEFINITION Sequence 59 from Patent EP1016715.  
 ACCESSION AX032613  
 VERSION AX032613.1 GI:110279551  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unclassified sequences.  
 REFERENCE 1  
 AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J., Bennett,C.P., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and Wyatt,J.R.  
 TITLE Oligonucleotides having a conserved G4 core sequence  
 JOURNAL Patent: EP 1016715-A 59 05-JUL-2000;  
 ISIS PHARMACEUTICALS INC (US)  
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 Db 21 ATCAACTCTGGAGTCCTCTG 1  
 RESULT 5  
 BD185713  
 LOCUS BD185713 22 bp DNA linear PAT 17-JUN-2003  
 DEFINITION Application of KIAA0172 gene functions for therapeutics, diagnosis, and pharmaceuticals.  
 ACCESSION BD185713  
 VERSION BD185713.1 GI:31877913  
 KEYWORDS JP 2002369696-A/14.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS Kiyama,R., Kitajima,K., Oguchi,S., Oishi,M., Ohara,O. and Nagase,T.  
 TITLE Application of KIAA0172 gene functions for therapeutics, diagnosis, and pharmaceuticals  
 JOURNAL Patent: JP 2002369696-A 14 24-DEC-2002;  
 NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, INFO GENES CO LTD, KAZUSA DNA RESEARCH INSTITUTE

COMMENT  
 OS Artificial Sequence  
 PN JP 2002369696-A/14  
 PD 24-DEC-2002  
 PF 01-APR-2002 JP 2002099422  
 PI RYOICHI KIYAMA, KEISUKE KITAJIMA, SHINOBU OGUCHI, MICHIO OISHI, O사무 OHARA,  
 PI TAKAHIRO NAGASE  
 PC C12N15/09,A61K31/711,A61K35/76,A61K38/00,A61K48/00,A61P35/00,  
 PC C12Q1/68,  
 G01N33/48,G01N33/53,G01N33/566,G01N33/574,G01N33/574, PC  
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 PC A61K37/02  
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 Best Local Similarity 94.1%; Pred. No. 14;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 60 AGCTGATGCTCTGTCAA 76  
 Db 2 AGCTGATGCTGTCAA 18  
 RESULT 6  
 BD089289/c  
 LOCUS BD089289 20 bp DNA linear PAT 27-AUG-2002  
 DEFINITION A method of arraying genome clone.  
 ACCESSION BD089289  
 VERSION BD089289.1 GI:22634899  
 KEYWORDS JP 2001321190-A/1533.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Soeda,E.  
 TITLE A method of arraying genome clone  
 JOURNAL Patent: JP 2001321190-A 1533 20-NOV-2001;  
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA GENOTECHS  
 COMMENT  
 OS Artificial Sequence  
 PN JP 2001321190-A/1533  
 PD 20-NOV-2001  
 PF 12-MAR-2001 JP 2001068285  
 PI EIICHI SOEDA  
 PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC  
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 Db 18 TGAAGAGCCAGCGAAGCT 1

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DEFINITION Sequence 3 from patent US 6448020.
ACCESSION AR228291
VERSION AR228291.1 GI:27267057
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Toftgard,R., Zaphiropoulos,P.G., Kogerman,P. and Grimm,T.
TITLE Molecules associated with the human suppressor of fused gene
JOURNAL Patent: US 6448020-A 3 10-SEP-2002;
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Best Local Similarity 88.9%; Pred. No. 17;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGAGTCTCTGTCA 75
Db 1 GAAGCTGAGTACTGCCA 18

RESULT 8
LOCUS CO625286
DEFINITION Sequence 10026 from Patent WO0192524.
ACCESSION CO625286
VERSION CO625286.1 GI:41675504
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 10026 06-DEC-2001;
FEATURES
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Best Local Similarity 93.8%; Pred. No. 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGTGAG 42
Db 2 TCTGGAGTCTCTGTG 17

RESULT 9
LOCUS CO625287
DEFINITION Sequence 10027 from Patent WO0192524.
ACCESSION CO625287
VERSION CO625287.1 GI:41675505
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 10027 03-FEB-2004;
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Best Local Similarity 93.8%; Pred. No. 17;
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RESULT 10
LOCUS AR466349
DEFINITION Sequence 10026 from patent US 6686188.
ACCESSION AR466349
VERSION AR466349.1 GI:42701406
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 10026 03-FEB-2004;
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Best Local Similarity 93.8%; Pred. No. 17;
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QY 27 TCTGGAGTCTCTGTGAG 42
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RESULT 11
LOCUS AR466350
DEFINITION Sequence 10027 from patent US 6686188.
ACCESSION AR466350
VERSION AR466350.1 GI:42701407
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 10027 03-FEB-2004;
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Best Local Similarity 93.8%; Pred. No. 17;
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QY 27 TCTGGAGTCTCTGTGAG 42
Db 2 TCTGGAGTCTCTGTG 17

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 10027 06-DEC-2001;
Aeomica, Inc. (US)
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QY 27 TCTGGAGTCTCTGTGAG 42
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RESULT 10
LOCUS AR466349
DEFINITION Sequence 10026 from patent US 6686188.
ACCESSION AR466349
VERSION AR466349.1 GI:42701406
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 10026 03-FEB-2004;
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Best Local Similarity 93.8%; Pred. No. 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGTGAG 42
Db 1 TCTGGAGTCTCTGTG 16

RESULT 11
LOCUS AR466350
DEFINITION Sequence 10027 from patent US 6686188.
ACCESSION AR466350
VERSION AR466350.1 GI:42701407
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 10027 03-FEB-2004;
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Best Local Similarity 93.8%; Pred. No. 17;
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  SOURCE
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 18)
    Cowsett,L.M.
  TITLE
    Antisense modulation of G-alpha-13 expression
  JOURNAL
    Patent: US 5981732-A 40 09-NOV-1999;
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Db 17 CCTGGGGAGACAAC 2

RESULT 13
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LOCUS
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  ACCESSION
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  VERSION
    CQ625284.1 GI:41675502
  KEYWORDS
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  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homiidae; Homo.
  REFERENCE
    1
    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
    Shannon,M.E.
  TITLE
    Myosin-like gene expressed in human heart and muscle
  JOURNAL
    Patent: WO 0192524-A 10024 06-DEC-2001;
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RESULT 16
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LOCUS
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    AR466348
  VERSION
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  VERSION
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  ORGANISM
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    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homiidae; Homo.
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    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
    Shannon,M.E.
  TITLE
    Myosin-like gene expressed in human heart and muscle
  JOURNAL
    Patent: WO 0192524-A 10025 06-DEC-2001;
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Db 3 TCTGGAGTCTCTCTG 16

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    AR466347.1 GI:42701404
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  REFERENCE
    1 (bases 1 to 17)
    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
    Shannon,M.E.
  TITLE
    Polynucleotide encoding a human myosin-like polypeptide expressed
    predominantly in heart and muscle
  JOURNAL
    Patent: US 6686188-A 10024 03-FEB-2004;
    Amersham PLC; Buckinghamshire;
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RESULT 16
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**KEYWORDS**  
 SOURCE Unknown.  
 ORGANISM Unknown.  
**REFERENCE**  
 1 (bases 1 to 17)  
**AUTHORS**  
 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
**TITLE**  
 Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
**JOURNAL**  
 Patent: US 6686188-A 10025 03-FEB-2004;  
 Amer sham PLC; Buckinghamshire;  
 GBX;  
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**Db**  
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 LOCUS AX649090 17 bp DNA linear PAT 22-MAR-2003  
 DEFINITION Sequence 930 from Patent EP1273660.  
 ACCESSION AX649090  
 VERSION AX649090.1 GI:29151908  
 KEYWORDS  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.  
**REFERENCE**  
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**AUTHORS**  
 Gu, Y.  
**TITLE**  
 Human sodium-hydrogen exchanger like protein 1  
**JOURNAL**  
 Patent: EP 1273660-A 930 08-JAN-2003;  
 Aeomica, Inc. (US)  
**FEATURES**  
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 17 AATGAGCCGCGAGAT 1  
**Db**  
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 CQ625288  
 LOCUS CQ625288 17 bp DNA linear PAT 02-FEB-2004  
 DEFINITION Sequence 10028 from Patent WO0192524.  
 ACCESSION CQ625288  
 VERSION CQ625288.1 GI:41675506  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.  
**REFERENCE**  
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**AUTHORS**  
 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
**KEYWORDS**  
 SOURCE Unknown.  
 ORGANISM Unknown.  
**REFERENCE**  
 1 (bases 1 to 17)  
**AUTHORS**  
 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
**TITLE**  
 Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
**JOURNAL**  
 Patent: US 6686188-A 10025 03-FEB-2004;  
 Amer sham PLC; Buckinghamshire;  
 GBX;  
**FEATURES**  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 26;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
**Qy**  
 28 CTGGAGTCTCTGAG 42  
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 1 CTGGAGTCTCTGTG 15  
**Db**  
**RESULT 19**  
 AR466351  
 LOCUS AR466351 17 bp DNA linear PAT 20-FEB-2004  
 DEFINITION Sequence 10028 from patent US 6686188.  
 ACCESSION AR466351  
 VERSION AR466351.1 GI:42701408  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
**REFERENCE**  
 1 (bases 1 to 17)  
**AUTHORS**  
 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
**TITLE**  
 Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
**JOURNAL**  
 Patent: US 6686188-A 10028 03-FEB-2004;  
 Amer sham PLC; Buckinghamshire;  
 GBX;  
**FEATURES**  
 source Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 26;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
**Qy**  
 28 CTGGAGTCTCTGAG 42  
 |||||  
 1 CTGGAGTCTCTGTG 15  
**Db**  
**RESULT 20**  
 AX649091/c  
 LOCUS AX649091 17 bp DNA linear PAT 22-MAR-2003  
 DEFINITION Sequence 931 from Patent EP1273660.  
 ACCESSION AX649091  
 VERSION AX649091.1 GI:29151909  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.  
**REFERENCE**  
 1  
**AUTHORS**  
 Gu, Y.  
**TITLE**  
 Human sodium-hydrogen exchanger like protein 1  
**JOURNAL**  
 Patent: EP 1273660-A 931 08-JAN-2003;  
 Aeomica, Inc. (US)  
**FEATURES**  
 source Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 26;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAG 61  
 DB 16 AATGAGCCAGCGAAG 2

RESULT 21  
 AX649092/c  
 LOCUS  
 DEFINITION Sequence 932 from Patent EP1273660.  
 ACCESSION AX649092  
 VERSION AX649092.1 GI:29151910  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

AX649092 17 bp DNA linear PAT 22-MAR-2003  
 Sequence 932 from Patent EP1273660.  
 AX649092  
 AX649092.1 GI:29151910  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE 1  
 AUTHORS Gu, Y.  
 TITLE Human sodium-hydrogen exchanger like protein 1  
 JOURNAL Patent: EP 1273660-A 932 08-JAN-2003;  
 Acomica, Inc. (US)

FEATURES  
 source  
 1. .17  
 Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 26;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAG 61  
 DB 15 AATGAGCCAGCGAAG 1

RESULT 22  
 AX674032/c  
 LOCUS  
 DEFINITION Sequence 2477 from Patent WO03004526.  
 ACCESSION AX674032  
 VERSION AX674032.1 GI:29332380  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

AX674032 17 bp DNA linear PAT 27-MAR-2003  
 Sequence 2477 from Patent WO03004526.  
 AX674032  
 AX674032.1 GI:29332380  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE 1  
 AUTHORS Telesman, A., Anson, R. and Tuijnder, M.  
 TITLE Sequences involved in phenomena of tumour suppression, tumour  
 reversion, apoptosis and/or resistance to viruses and their use as  
 medicines  
 JOURNAL Patent: WO 03004526-A 2477 16-JAN-2003;  
 Molecular Engines Laboratories (FR)

FEATURES  
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 Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 26;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCTCTGAGA 43  
 DB 17 TGGAGTCTCTGAGA 3

RESULT 23  
 AX732023/c  
 LOCUS  
 DEFINITION Sequence 3657 from Patent WO03025175.  
 ACCESSION AX732023  
 VERSION AX732023.1 GI:30511366  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

AX732023 17 bp DNA linear PAT 08-MAY-2003  
 Sequence 3657 from Patent WO03025175.  
 AX732023  
 AX732023.1 GI:30511366  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE 1  
 AUTHORS Telesman, A., Anson, R. and Tuijnder, M.  
 TITLE Sequences involved in phenomena of tumour suppression, tumour  
 reversion, apoptosis and/or virus resistance and their use as  
 medicines  
 JOURNAL Patent: WO 03025175-A 3657 27-MAR-2003;  
 Molecular Engines Laboratories (FR)

FEATURES  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 26;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCTCTGAGA 43  
 DB 17 TGGAGTCTCTGAGA 3

RESULT 24  
 AX738057/c  
 LOCUS  
 DEFINITION Sequence 3647 from Patent WO03025177.  
 ACCESSION AX738057  
 VERSION AX738057.1 GI:30517345  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

AX738057 17 bp DNA linear PAT 08-MAY-2003  
 Sequence 3647 from Patent WO03025177.  
 AX738057  
 AX738057.1 GI:30517345  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE 1  
 AUTHORS Telesman, A., Anson, R. and Tuijnder, M.  
 TITLE Sequences involved in phenomena of tumour suppression, tumour  
 reversion, apoptosis and/or resistance to viruses and the use  
 thereof as medicaments  
 JOURNAL Patent: WO 03025177-A 3647 27-MAR-2003;  
 Molecular Engines Laboratories (FR)

FEATURES  
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 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 26;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCTCTGAGA 43  
 DB 17 TGGAGTCTCTGAGA 3

RESULT 25  
 AX762421/c  
 LOCUS  
 AX762421 17 bp DNA linear PAT 25-JUN-2003

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DEFINITION      Sequence 5742 from Patent WO03040369.
ACCESSION       AX762421
VERSION         AX762421.1 GI:32257037
KEYWORDS        Homo sapiens (human)
SOURCE          Homo sapiens
ORGANISM        Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homiidae; Homo.
REFERENCE       1
AUTHORS         Telerman,A., Anson,R. and Tuijnder,M.
TITLE           Sequences involved in tumoral suppression, tumoral reversion,
                apoptosis and/or viral resistance phenomena and their use as
                medicines
JOURNAL         Patent: WO 03040369-A 5742 15-MAY-2003;
                Molecular Engines Laboratories (FR)
FEATURES        Location/Qualifiers
                source
                1..17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match    17.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 29 TGGAGTCTCTGAGA 43
Db 17 TGGAGTCTCTGAGA 3

RESULT 26
AR166421/c
LOCUS          AR166421      18 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION     Sequence 14 from patent US 6280998.
ACCESSION      AR166421
VERSION        AR166421.1 GI:16241735
KEYWORDS       Unknown.
SOURCE         Unclassified.
ORGANISM       1 (bases 1 to 18)
REFERENCE      Mathur,E.J., Marsh,E.J. and Schoettlin,W.E.
AUTHORS        Purified thermostable pyrococcus furiosus DNA ligase
TITLE          Patent: US 6280998-A 14 28-AUG-2001;
JOURNAL        Location/Qualifiers
FEATURES        source
                1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACAACTTGGAGTC 1

RESULT 27
AR166424
LOCUS          AR166424      18 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION     Sequence 17 from patent US 6280998.
ACCESSION      AR166424
VERSION        AR166424.1 GI:16241740
KEYWORDS       Unknown.
SOURCE         Unclassified.
ORGANISM       1 (bases 1 to 18)
REFERENCE      Mathur,E.J., Marsh,E.J. and Schoettlin,W.E.
AUTHORS        Purified thermostable pyrococcus furiosus DNA ligase
TITLE          Patent: US 6280998-A 17 28-AUG-2001;
JOURNAL        Location/Qualifiers
FEATURES        source
                1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACAACTTGGAGTC 1

RESULT 28
AR166424
LOCUS          AR166424      18 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION     Sequence 17 from patent US 6280998.
ACCESSION      AR166424
VERSION        AR166424.1 GI:16241740
KEYWORDS       Unknown.
SOURCE         Unclassified.
ORGANISM       1 (bases 1 to 18)
REFERENCE      Mathur,E.J., Marsh,E.J. and Schoettlin,W.E.
AUTHORS        Purified thermostable pyrococcus furiosus DNA ligase
TITLE          Patent: US 6280998-A 17 28-AUG-2001;
JOURNAL        Location/Qualifiers
FEATURES        source
                1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACAACTTGGAGTC 1

RESULT 29
AR16540
LOCUS          AR16540      18 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION     Sequence 17 from patent US 5506137.
ACCESSION      AR16540
VERSION        AR16540.1 GI:1599895
KEYWORDS       Unknown.
SOURCE         Unclassified.
ORGANISM       1 (bases 1 to 18)
REFERENCE      Mathur,E.J., Marsh,E.J. and Schoettlin,W.E.
AUTHORS        Purified thermostable Pyrococcus furiosus DNA ligase
TITLE          Patent: US 5506137-A 17 09-APR-1996;
JOURNAL        Location/Qualifiers
FEATURES        source
                1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACAACTTGGAGTC 1

RESULT 30
AR16217/c
LOCUS          AR16217      18 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION     Sequence 14 from patent US 5506137.
ACCESSION      AR16217
VERSION        AR16217.1 GI:1599892
KEYWORDS       Unknown.
SOURCE         Unclassified.
ORGANISM       1 (bases 1 to 18)
REFERENCE      Mathur,E.J., Marsh,E.J. and Schoettlin,W.E.
AUTHORS        Purified thermostable Pyrococcus furiosus DNA ligase
TITLE          Patent: US 5506137-A 14 09-APR-1996;
JOURNAL        Location/Qualifiers
FEATURES        source
                1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACAACTTGGAGTC 18

RESULT 31
AR16217/c
LOCUS          AR16217      18 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION     Sequence 14 from patent US 5506137.
ACCESSION      AR16217
VERSION        AR16217.1 GI:1599892
KEYWORDS       Unknown.
SOURCE         Unclassified.
ORGANISM       1 (bases 1 to 18)
REFERENCE      Mathur,E.J., Marsh,E.J. and Schoettlin,W.E.
AUTHORS        Purified thermostable Pyrococcus furiosus DNA ligase
TITLE          Patent: US 5506137-A 14 09-APR-1996;
JOURNAL        Location/Qualifiers
FEATURES        source
                1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACAACTTGGAGTC 18

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Query Match	17.1%;	Score 13.2;	DB 1;	Length 18;	
Best Local Similarity	83.3%;	Pred. No. 29;			
Matches	15;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	30	GGAGTCCTCTGAGAGGTA	47		
Db	18	GGAGTCGTAGGAGGTA	1		
RESULT 33					
AX207952/c					
LOCUS	AX207952	18 bp	DNA	linear	PAT 31-AUG-2001
DEFINITION	Sequence 56 from Patent WO0157194.				
ACCESSION	AX207952				
VERSION	AX207952.1	GI:15422550			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1				
AUTHORS	Madison,E.L., Ong,E.O. and Yeh,J.C.				
TITLE	Nucleic acid molecules encoding transmembrane serine proteases, the encoded proteins and methods based thereon				
JOURNAL	Patent: WO 0157194-A 56 09-AUG-2001;				
	CORVAS INTERNATIONAL, INC. (US)				
FEATURES	Location/Qualifiers				
source	1..18				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Oligonucleotide Primer"				
Query Match	17.1%;	Score 13.2;	DB 1;	Length 18;	
Best Local Similarity	83.3%;	Pred. No. 29;			
Matches	15;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	30	GGAGTCCTCTGAGAGGTA	47		
Db	18	GGAGTCGTAGGAGGTA	1		
RESULT 34					
AX473057/c					
LOCUS	AX473057	18 bp	DNA	linear	PAT 09-AUG-2002
DEFINITION	Sequence 6 from Patent WO0220475.				
ACCESSION	AX473057				
VERSION	AX473057.1	GI:22207820			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1				
AUTHORS	Duncan,D.F., Madison,E.L., Semple,J.E., Combs,G.S., Reiner,J.E., Ong,E.O. and Araldi,G.L.				
TITLE	Inhibitors of serine protease activity of matriptase or mcspl				
JOURNAL	Patent: WO 0220475-A 6 14-MAR-2002;				
	CORVAS INTERNATIONAL, INC. (US)				
FEATURES	Location/Qualifiers				
source	1..18				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="oligonucleotide primer"				
Query Match	17.1%;	Score 13.2;	DB 1;	Length 18;	
Best Local Similarity	83.3%;	Pred. No. 29;			
Matches	15;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	30	GGAGTCCTCTGAGAGGTA	47		
Db	18	GGAGTCGTAGGAGGTA	1		

RESULT 35  
CO625283  
LOCUS AX649089/c 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 10023 from Patent WO0192524.  
ACCESSION CO625283  
VERSION CO625283.1 GI:41675501  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 10023 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 16.9%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 TCTGGAGTCTCTCT 39  
Db 5 TCTGGAGTCTCTCT 17

RESULT 36  
AR466346  
LOCUS AR466346 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 10023 from patent US 6686188.  
ACCESSION AR466346  
VERSION AR466346.1 GI:42701403  
KEYWORDS Unknown.  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 10023 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source 1..17  
Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 16.9%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 TCTGGAGTCTCTCT 39  
Db 5 TCTGGAGTCTCTCT 17

RESULT 37  
AX649089/c  
LOCUS AX649089 17 bp DNA linear PAT 22-MAR-2003  
DEFINITION Sequence 929 from Patent EP1273660.  
ACCESSION AX649089  
VERSION AX649089.1 GI:29151907  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Gu, Y.  
TITLE Human sodium-hydrogen exchanger like protein 1  
JOURNAL Patent: EP 1273660-A 929 08-JAN-2003;  
Aeomica, Inc. (US)  
FEATURES  
source 1..17  
Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 16.6%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 33;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 48 AAGAGCCAGCGAGCT 63  
Db 17 ATGAGCCAGCGAAGAT 2

RESULT 38  
AX762338/c  
LOCUS AX762338 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 5659 from Patent WO03040369.  
ACCESSION AX762338  
VERSION AX762338.1 GI:32256954  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
JOURNAL Patent: WO 03040369-A 5659 15-MAY-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source 1..17  
Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 16.6%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 33;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 6 AAGACGGCTCTGGGGAT 21  
Db 17 AAGGCTGCTCTGGGGAT 2

RESULT 39  
CO625289  
LOCUS CO625289 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 10029 from Patent WO0192524.  
ACCESSION CO625289  
VERSION CO625289.1 GI:41675507  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and

Shannon, M.E.  
 Myosin-like gene expressed in human heart and muscle  
 Patent: WO 0192524-A 10029 06-DEC-2001;  
 Aeomica, Inc. (US)  
 FEATURES  
 source  
 1. .17  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 38;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 29 TGGAGTCCTCTGAG 42  
 Db 1 TGGAGTCCTCTGTG 14

RESULT 40  
 AR286445  
 LOCUS  
 DEFINITION Sequence 817 from patent US 6528640.  
 ACCESSION AR286445  
 VERSION AR286445.1 GI:29724041  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Beigelman, L., Burgin, A., Beaudry, A., Karpelsky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.  
 TITLE Synthetic ribonucleic acids with RNase activity  
 JOURNAL  
 FEATURES  
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 1. .17  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 38;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGGAGTCCTCTGA 41  
 Db 4 CTGGAGCCCTCTGA 17

RESULT 41  
 AR398435  
 LOCUS  
 DEFINITION Sequence 816 from patent US 6617438.  
 ACCESSION AR398435  
 VERSION AR398435.1 GI:40136245  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Beigelman, L., Burgin, A.B., Beaudry, A., Karpelsky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.  
 TITLE Oligoribonucleotides with enzymatic activity  
 JOURNAL  
 FEATURES  
 source  
 1. .17  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 38;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGGAGTCCTCTGA 41  
 Db 4 CTGGAGCCCTCTGA 17

RESULT 41  
 AR398435  
 LOCUS  
 DEFINITION Sequence 816 from patent US 6617438.  
 ACCESSION AR398435  
 VERSION AR398435.1 GI:40136245  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Beigelman, L., Burgin, A.B., Beaudry, A., Karpelsky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.  
 TITLE Oligoribonucleotides with enzymatic activity  
 JOURNAL  
 FEATURES  
 source  
 1. .17  
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 /mol\_type="unassigned RNA"

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 38;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGGAGTCCTCTGA 41  
 Db 4 CTGGAGCCCTCTGA 17

RESULT 42  
 AR466352  
 LOCUS  
 DEFINITION Sequence 10029 from patent US 6686188.  
 ACCESSION AR466352  
 VERSION AR466352.1 GI:42701409  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
 JOURNAL  
 Patent: US 6686188-A 10029 03-FEB-2004;  
 Amer sham PLC; Buckinghamshire;  
 GBX;  
 FEATURES  
 source  
 1. .17  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 38;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 29 TGGAGTCCTCTGAG 42  
 Db 1 TGGAGTCCTCTGTG 14

RESULT 43  
 AX649087/c  
 LOCUS  
 DEFINITION Sequence 927 from Patent EPI273660.  
 ACCESSION AX649087  
 VERSION AX649087.1 GI:29151905  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Gu, Y.  
 TITLE Human sodium-hydrogen exchanger like protein 1  
 JOURNAL  
 Patent: EP 1273660-A 927 08-JAN-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
 source  
 1. .17  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 38;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAGCT 53  
 Db 17 GAGCCAGCGAAGAT 4

RESULT 44  
 AX649088/c  
 LOCUS

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DEFINITION Sequence 928 from Patent EP1273660.
ACCESSION AX649088
VERSION AX649088.1 GI:29151906
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Gu, Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 928 08-JAN-2003;
JOURNAL Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 38;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAAGCT 63
Db 16 GAGCCAGCGAAGAT 3

RESULT 45
ACCESSION AX649093/c
LOCUS AX649093
DEFINITION Sequence 933 from Patent EP1273660.
ACCESSION AX649093
VERSION AX649093.1 GI:29151911
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Gu, Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 933 08-JAN-2003;
JOURNAL Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 38;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAGAGCCAGCGAA 60
Db 14 AATGAGCCAGCGAA 1

RESULT 46
ACCESSION AX734726
LOCUS AX734726
DEFINITION Sequence 316 from Patent WO03025177.
ACCESSION AX734726
VERSION AX734726.1 GI:30514003
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

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```

REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 316 27-MAR-2003;
JOURNAL Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 38;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCTG 40
Db 3 TCTGGTGTCTCTCTG 16

RESULT 47
ACCESSION BD203204/c
LOCUS BD203204
DEFINITION Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION BD203204
VERSION BD203204.1 GI:33012974
KEYWORDS JP 2002509721-A/6230.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
TITLE Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 6230 02-APR-2002;
JOURNAL RIBOSYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/6230
PD 02-APR-2002
PR 24-MAR-1999 JP 2000541291
PI 27-MAR-1998 US 60/079678
PI PANELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
PC A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
CC concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT /organism="Homo sapiens (human)".
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1. .17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 16 GGGGATACACTCTGGA 32
Db 17 GGGGGTATTACTCTGGA 1

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RESULT 48
AX687578/c
LOCUS AX687578 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 310 from Patent EP1281758.
ACCESSION AX687578
VERSION AX687578.1 GI:29410274
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 310 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. .17
Location/Qualifiers
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 28 CTGGAGTCTCTGAGAG 44
Db 17 CTGGAGCCCCCTAGAG 1

RESULT 49
AX727379
LOCUS AX727379 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5066 from Patent WO03025176.
ACCESSION AX727379
VERSION AX727379.1 GI:30506722
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS Teleman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 5066 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
Location/Qualifiers
/mol_type="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 50 GAGCCAGGAGCTGAT 66
Db 1 GATCCAGGAGCTGAT 17

RESULT 50
CQ858651
LOCUS CQ858651 16 bp DNA linear PAT 31-AUG-2004
DEFINITION Sequence 113 from Patent WO2004069991.
ACCESSION CQ858651

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CQ858651.1 GI:51852618
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Hansen,B., Thruue,C.A., Petersen,K.D., Westergaard,M. and Wissenbach,M.
TITLE Oligomeric compounds for the modulation of survivin expression
JOURNAL Patent: WO 2004069991-A 113 19-AUG-2004;
Santaris Pharma A/S (DK)
FEATURES
Location/Qualifiers
source
1. .16
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64
Db 4 CCAGCGAAGCTG 15

RESULT 51
CQ625282
LOCUS CQ625282 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 10022 from Patent WO0192524.
ACCESSION CQ625282
VERSION CQ625282.1 GI:41675500
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 10022 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers
source
1. .17
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 15.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCTCTC 38
Db 6 TCTGGAGTCTCTC 17

RESULT 52
AR466345
LOCUS AR466345 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 10022 from patent US 6686188.
ACCESSION AR466345
VERSION AR466345.1 GI:42701402
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and

```

Shannon,M.E.  
 Polynucleotide encoding a human myosin-like polypeptide expressed  
 predominantly in heart and muscle  
 Patent: US 5686188-A 10022 03-FEB-2004;  
 AmerSham PLC; Buckinghamshire;  
 GBX;

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 1. .17  
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 /mol\_type="genomic DNA"  
 Query Match 15.6%; Score 12; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 27 TCTGGAGTCCTC 38  
 Db 6 TCTGGAGTCCTC 17

RESULT 53  
 AR329584/c  
 LOCUS AR329584 16 bp RNA linear PAT 17-AUG-2003  
 DEFINITION Sequence 6986 from patent US 5686127.  
 ACCESSION AR329584  
 VERSION AR329584.1 GI:33715392  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
 TITLE Method and reagent for the treatment of diseases or conditions  
 related to levels of vascular endothelial growth factor receptor  
 JOURNAL Patent: US 5686127-A 6986 20-MAY-2003;  
 Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
 FEATURES  
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 1. .16  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

Query Match 15.3%; Score 11.8; DB 1; Length 16;  
 Best Local Similarity 86.7%; Pred. No. 46;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 52 GCCAGCGAGCTGAT 66  
 Db 16 GCCAGCATAGCTGAT 2

RESULT 54  
 AR362384/c  
 LOCUS AR362384 16 bp DNA linear PAT 03-SEP-2003  
 DEFINITION Sequence 12 from patent US 5168062.  
 ACCESSION AR362384  
 VERSION AR362384.1 GI:34422357  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Stinski,M.F.  
 TITLE Transfer vectors and microorganisms containing human  
 cytomegalovirus immediate-early promoter-regulatory DNA sequence  
 JOURNAL Patent: US 5168062-A 12 01-DEC-1992;  
 University of Iowa Research Foundation; Oakdale, IA;  
 EPX;

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 source  
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 /mol\_type="genomic DNA"  
 Query Match 15.3%; Score 11.8; DB 1; Length 16;

Best Local Similarity 86.7%; Pred. No. 46;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 63 TGATGTCCTGTCAAG 77  
 Db 15 TGATGACTGCCAAG 1

RESULT 55  
 AR362385/c  
 LOCUS AR362385 16 bp DNA linear PAT 03-SEP-2003  
 DEFINITION Sequence 13 from patent US 5168062.  
 ACCESSION AR362385  
 VERSION AR362385.1 GI:34422358  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Stinski,M.F.  
 TITLE Transfer vectors and microorganisms containing human  
 cytomegalovirus immediate-early promoter-regulatory DNA sequence  
 JOURNAL Patent: US 5168062-A 13 01-DEC-1992;  
 University of Iowa Research Foundation; Oakdale, IA;  
 EPX;  
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 source  
 1. .16  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 15.3%; Score 11.8; DB 1; Length 16;  
 Best Local Similarity 86.7%; Pred. No. 46;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 63 TGATGTCCTGTCAAG 77  
 Db 15 TGATGACTGCCAAG 1

RESULT 56  
 AR029815/c  
 LOCUS AR029815 16 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 4 from patent US 5861244.  
 ACCESSION AR029815  
 VERSION AR029815.1 GI:5943029  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Wang,C.-G. and Hepburn,A.G.  
 TITLE Genetic sequence assay using DNA triple strand formation  
 JOURNAL Patent: US 5861244-A 4 19-JAN-1999;  
 Location/Qualifiers  
 source  
 1. .16  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 14.8%; Score 11.4; DB 1; Length 16;  
 Best Local Similarity 92.3%; Pred. No. 53;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 40 GAGAGGTAAGAG 52  
 Db 14 GAGAGGTAAGAG 2

RESULT 57  
 BD106403  
 LOCUS BD106403 16 bp DNA linear PAT 18-SEP-2002  
 DEFINITION Novel LDL-receptor.  
 ACCESSION BD106403  
 VERSION BD106403.1 GI:23201221

KEYWORDS JP 2002501376-A/418.  
SOURCE Chlamydia sp.  
ORGANISM Chlamydia sp.  
REFERENCE Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
AUTHORS 1 (bases 1 to 16)  
TODD, J.A., HESS, J.W., CASKEY, C.T., COX, R.D., GERHOLD, D.,  
and HEY, P.  
TITLE Novel LDI-receptor  
JOURNAL Patent: JP 2002501376-A 418 15-JAN-2002;  
THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO  
INC  
COMMENT PN JP 2002501376-A/418  
PD 15-JAN-2002  
PF 15-JAN-1998 JP 1998543635  
PR 15-APR-1997 US 60/043553, 05-JUN-1997 US 60/048740 PI  
JOHN ANDREW TODD, JOHN WILFRED HESS, CHARLES  
THOMAS CASKEY, ROGER  
PI DAVID COX.  
PC C12N15/12, C12N15/11, C12Q1/68, C07K14/705, C07K16/28, A61K38/17,  
A61K39/395,  
A61K48/00  
PC A61K39/395,  
A61K48/00  
CC Strandedness: Double;  
CC Topology: Linear;  
PH Key Location/Qualifiers.  
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Source 1. .16  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:35827"  
Query Match 14.5%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 58;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 39 TGAGAGGTAAGAGCC 54  
Db 1 TCACAGGTAAGAGCC 16  
RESULT 58  
LOCUS 118626 16 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 12 from patent US 5500341.  
ACCESSION 118626  
VERSION 118626.1 GI:1598981  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Spears, P.A.  
TITLE Species-specific detection of Mycobacterium kansasii  
JOURNAL Patent: US 5500341-A 12 19-MAR-1996;  
FEATURES  
Source 1. .16  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 14.5%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 58;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 AACACAGCGCGCTGGG 18  
Db 1 AACTCGAGCGCGCTCGG 16  
RESULT 59  
LOCUS AR305492 16 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 450 from patent US 6545137.  
ACCESSION AR305492

VERSION AR305492.1 GI:31694802  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D.,  
Hammond, H., Hey, P., Kawaguchi, Y., Merriman, T.R., Metzker, M.L.,  
Nakagawa, Y., Phillips, M.S. and Twells, R.C.J.  
TITLE Receptor  
JOURNAL Patent: US 6545137-A 450 08-APR-2003;  
FEATURES  
Source 1. .16  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 14.5%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 58;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 39 TGAGAGGTAAGAGCC 54  
Db 1 TCACAGGTAAGAGCC 16  
RESULT 60  
LOCUS AR309596 16 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 450 from patent US 6555654.  
ACCESSION AR309596  
VERSION AR309596.1 GI:31701601  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D.,  
Hammond, H., Hey, P., Kawaguchi, Y., Merriman, T.R., Metzker, M.L.,  
Nakagawa, Y., Phillips, M.S. and Twells, R.C.J.  
TITLE LDL-receptor  
JOURNAL Patent: US 6555654-A 450 29-APR-2003;  
The Wellcome Trust Limited as Trustee for the Wellcome Trust;  
London;  
WOX;  
FEATURES  
Source 1. .16  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 14.5%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 58;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 39 TGAGAGGTAAGAGCC 54  
Db 1 TCACAGGTAAGAGCC 16  
RESULT 61  
LOCUS AR455592/c 16 bp RNA linear PAT 20-FEB-2004  
DEFINITION Sequence 9 from patent US 6685948.  
ACCESSION AR455592  
VERSION AR455592.1 GI:42690466  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Zeng, L. and Markoff, L.  
TITLE Replication-defective dengue viruses that are replication-defective  
in mosquitoes for use as vaccines  
JOURNAL Patent: US 6685948-A 9 03-FEB-2004;

The United States of America as represented by the Department of Health and Human Services; Washington, DC;  
WOX;

FEATURES  
source  
1. .16  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 14.5%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 58;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 26 CTCTGGAGTCTCTGA 41  
Db 16 CTCTGTGTCTATGA 1

RESULT 62  
LOCUS AR630011/c 16 bp DNA linear PAT 14-FEB-2005  
DEFINITION Sequence 65 from patent US 6838556.  
ACCESSION AR630011  
VERSION AR630011.1 GI:59762202  
KEYWORDS Unknown.  
SOURCE Unknown.

ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,  
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,  
Sheppard,L.T., Kim,M.Y. and Bruiice,T.W.

TITLE Promoters for regulated gene expression  
JOURNAL Patent: US 6838556-A 65 04-JAN-2005;  
Genelabs Technologies, Inc.; Redwood City, CA

FEATURES  
source  
1. .16  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 14.5%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 58;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 38 CTGAGAGGTAAGAGC 53  
Db 16 CTGGAGGTGGAGC 1

RESULT 63  
LOCUS AX351113/c 16 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 65 from Patent WO0194600.  
ACCESSION AX351113  
VERSION AX351113.1 GI:18616467

KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1  
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,  
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,  
Sheppard,L.T., Lim,M.Y. and Bruiice,T.W.

TITLE Promoters for regulated gene expression  
JOURNAL Patent: WO 0194600-A 65 13-DEC-2001;  
GENELABS TECHNOLOGIES, INC. (US)

FEATURES  
source  
1. .16  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 14.5%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 58;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 38 CTGAGAGGTAAGAGC 53  
Db 16 CTGGAGGTGGAGC 1

RESULT 64  
LOCUS AX552593/c 16 bp RNA linear PAT 27-NOV-2002  
DEFINITION Sequence 9 from Patent WO02074963.  
ACCESSION AX552593  
VERSION AX552593.1 GI:25896602  
KEYWORDS West Nile virus (WNV)  
SOURCE West Nile virus

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.

REFERENCE 1  
AUTHORS Markoff,L. and Zeng,L.  
TITLE Dengue viruses that are replication defective in mosquitos for use  
as vaccines

JOURNAL Patent: WO 02074963-A 9 26-SEP-2002;  
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES  
source  
1. .16  
Location/Qualifiers  
/organism="West Nile virus"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:11082"

Query Match 14.5%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 58;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 26 CTCTGGAGTCTCTGA 41  
Db 16 CTCTGTGTCTATGA 1

RESULT 65  
LOCUS AX927981/c 16 bp DNA linear PAT 19-DEC-2003  
DEFINITION Sequence 67 from Patent WO03085110.  
ACCESSION AX927981  
VERSION AX927981.1 GI:40250934

KEYWORDS synthetic construct  
SOURCE other sequences; artificial sequences.  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Thue,C.A., h G,A.M. and Kristjansen,P.E.  
TITLE Oligomeric compounds for the modulation hif-1alpha expression  
JOURNAL Patent: WO 03085110-A 67 16-OCT-2003;  
Cureon A/S (DK)

FEATURES  
source  
1. .16  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

/notes="Description of Artificial Sequence:antisense  
oligonucleotide to human HIF-1a"

Query Match 14.5%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 58;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAGC 62  
Db 16 AAACACACGCGAAGC 1

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RESULT 66
AX470971/c
LOCUS AX470971 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 548 from Patent WO02053773.
ACCESSION AX470971
VERSION AX470971.1 GI:22206096
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 548 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 20 ATCAACTCTG 30
Db 11 ATCAACTCTG 1
RESULT 67
AX624831/c
LOCUS AX624831 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1872 from Patent WO02053774.
ACCESSION AX624831
VERSION AX624831.1 GI:28452772
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1872 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 20 ATCAACTCTG 30
Db 11 ATCAACTCTG 1
RESULT 68
AX632252/c
LOCUS AX632252 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9294 from Patent WO02053774.
ACCESSION AX632252
VERSION AX632252.1 GI:28467867
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9294 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 20 ATCAACTCTG 30
Db 11 ATCAACTCTG 1
RESULT 69
AX587244
LOCUS AX587244 14 bp DNA linear PAT 10-JAN-2003
DEFINITION Sequence 20 from Patent WO0236761.
ACCESSION AX587244
VERSION AX587244.1 GI:27656109
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS D'Andrea,A.D., Taniguchi,T., Timmers,C. and Grompe,M.
TITLE Methods and compositions for the diagnosis of cancer
susceptibilities and defective dna repair mechanisms and treatment
thereof
JOURNAL Patent: WO 0236761-A 20 10-MAY-2002;
DANA FARBER CANCER INSTITUTE (US)
FEATURES
source
1. .14
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1. .14
note="Intron/Exon Junction of FANCD"
Query Match 14.3%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 43 AGGTAAGAGC 53
Db 2 AGGTAAGAGC 12
RESULT 70
BD208921/c
LOCUS BD208921 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD208921
VERSION BD208921.1 GI:33018691
KEYWORDS JP 2002512791-A/2511.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9294 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 20 ATCAACTCTG 30
Db 11 ATCAACTCTG 1
RESULT 69
AX587244
LOCUS AX587244 14 bp DNA linear PAT 10-JAN-2003
DEFINITION Sequence 20 from Patent WO0236761.
ACCESSION AX587244
VERSION AX587244.1 GI:27656109
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS D'Andrea,A.D., Taniguchi,T., Timmers,C. and Grompe,M.
TITLE Methods and compositions for the diagnosis of cancer
susceptibilities and defective dna repair mechanisms and treatment
thereof
JOURNAL Patent: WO 0236761-A 20 10-MAY-2002;
DANA FARBER CANCER INSTITUTE (US)
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1. .14
note="Intron/Exon Junction of FANCD"
Query Match 14.3%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 43 AGGTAAGAGC 53
Db 2 AGGTAAGAGC 12
RESULT 70
BD208921/c
LOCUS BD208921 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD208921
VERSION BD208921.1 GI:33018691
KEYWORDS JP 2002512791-A/2511.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related

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JOURNAL      to hepatitis C virus infection
Patent: JP 2002512791-A 2511 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Hepatitis virus (hepatitis C virus)
FN          JP 2002512791-A/2511
PD          08-MAY-2002
PF          26-APR-1999 JP 2000545991
PR          27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI          DENNIS MACEJAK
PC          C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC          A61K37/66,
PC          C12N15/00
CC          Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC          hepatitis C virus infection.
FH          Key Location/Qualifiers
FT          1. .15
FT          source /organism='Hepatitis virus (hepatitis C FT
virus)'
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source      Location/Qualifiers
1. .15
/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          45 GTAAAGAGCCA 55
DB          13 GTAAAGAGCCA 3
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RESULT 71
BD208922/c
LOCUS      BD208922 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD208922
VERSION BD208922.1 GI:33018692
KEYWORDS JP 2002512791-A/2512.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE      Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL    RIBOZYME PHARMACEUTICALS INC
Patent: JP 2002512791-A 2512 08-MAY-2002;
COMMENT    OS Hepatitis virus (hepatitis C virus)
FN          JP 2002512791-A/2512
PD          08-MAY-2002
PF          26-APR-1999 JP 2000545991
PR          27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI          DENNIS MACEJAK
PC          C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC          A61K37/66,
PC          C12N15/00
CC          Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC          hepatitis C virus infection.
FH          Key Location/Qualifiers
FT          1. .15
FT          source /organism='Hepatitis virus (hepatitis C FT
virus)'

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Query Match 14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          45 GTAAAGAGCCA 55
DB          11 GTAAAGAGCCA 1
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RESULT 72
A15668/c
LOCUS      A15668 14 bp DNA linear PAT 25-MAR-1994
DEFINITION oligonucleotide.
ACCESSION A15668
VERSION A15668.1 GI:512155
KEYWORDS .
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE 1 (bases 1 to 14)
AUTHORS Verrips,C.T., Maat,J., Edens,L. and Ledebor,A.M.
TITLE      Structural genes encoding the various allelic and maturation forms
of preprothaeumatin, recombinant cloning vehicles comprising said
structural genes and expression thereof in transformed microbial
host cells
JOURNAL    Patent: EP 0054331-A 4 23-JUN-1982;
UNILEVER NV; UNILEVER PLC
FEATURES
source      Location/Qualifiers
1. .14
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 14.0%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY          56 GCGAAGCTGATGTC 69
DB          14 GCGAAGCTGACGC 1
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RESULT 73
A15684
LOCUS      A15684 15 bp DNA linear PAT 25-MAR-1994
DEFINITION oligonucleotide.
ACCESSION A15684
VERSION A15684.1 GI:512743
KEYWORDS .
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Verrips,C.T., Maat,J., Edens,L. and Ledebor,A.M.
TITLE      Structural genes encoding the various allelic and maturation forms
of preprothaeumatin, recombinant cloning vehicles comprising said
structural genes and expression thereof in transformed microbial
host cells
JOURNAL    Patent: EP 0054331-A 20 23-JUN-1982;
UNILEVER NV; UNILEVER PLC
FEATURES
source      Location/Qualifiers
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/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 14.0%; Score 10.8; DB 1; Length 15;

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Best Local Similarity 85.7%; Pred. No. 64;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 56 GCGAAGCTGATGTC 69  
Db 1 GCGAAGCTGATGTC 14

RESULT 74  
AR033420/c  
LOCUS  
DEFINITION Sequence 186 from patent US 5869253.  
ACCESSION AR033420  
VERSION AR033420.1 GI:5949025  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Draper,K.G.  
TITLE Method and reagent for inhibiting hepatitis C virus replication  
JOURNAL Patent: US 5869253-A 186 09-FEB-1999;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 64;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGTC 70  
Db 15 CCAAGATGATGTC 2

RESULT 75  
AR113242/c  
LOCUS  
DEFINITION Sequence 186 from patent US 6132966.  
ACCESSION AR113242  
VERSION AR113242.1 GI:14093564  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Draper,K.G.  
TITLE Method and reagent for inhibiting hepatitis C virus replication  
JOURNAL Patent: US 6132966-A 186 17-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 64;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGTC 70  
Db 15 CCAAGATGATGTC 2

RESULT 76  
BD207153/c  
LOCUS  
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.  
ACCESSION BD207153  
VERSION BD207153.1 GI:33016923  
KEYWORDS JP 2002512791-A/743.  
SOURCE unidentified

ORGANISM unidentified  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.  
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection  
JOURNAL Patent: JP 2002512791-A 743 08-MAY-2002;  
COMMENT RIBOZYME PHARMACEUTICALS INC  
OS Hepatitis virus (hepatitis C virus)  
PN JP 2002512791-A/743  
PD 08-MAY-2002  
PF 26-APR-1999 JP 2000545991  
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR  
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI  
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI  
PAVCO,  
PI DENNIS MACEJAK  
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,  
PC A61K37/66,  
PC C12N15/00  
CC Enzymatic nucleic acid treatment of diseases or conditions related to  
CC hepatitis C virus infection.  
FH Key Location/Qualifiers  
FT source 1..15  
/organism="Hepatitis virus (hepatitis C virus)"  
/mol\_type="unassigned DNA"

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 64;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGTC 70  
Db 15 CCAAGATGATGTC 2

RESULT 77  
CS004710/c  
LOCUS  
DEFINITION Sequence 2738 from Patent EPI502950.  
ACCESSION CS004710  
VERSION CS004710.1 GI:58740065  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Stinchcomb,D.T., Chowrira,B., Drenzo,A., Draper,K.G., Dudycz,L.W., Grimm,S., Karpeisky,A., Kisch,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.  
TITLE Method for purifying chemically modified RNA  
JOURNAL Patent: EP 1502950-A 2738 02-FEB-2005;  
Ribozyne Pharmaceuticals, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 64;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 25 ACTCTGGATGTC 38  
Db 15 CCAAGATGATGTC 2

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Db      14 ACTCTGAAGTCTTC 1

RESULT 78
CS004712/c
LOCUS      15 bp      DNA      linear      PAT 07-FEB-2005
DEFINITION Sequence 2740 from Patent EPI502950.
ACCESSION CS004712
VERSION    CS004712.1 GI:58740067
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
           unclassified.
REFERENCE  1
AUTHORS    Stinchcomb,D.T., Chowira,B., Direnzo,A., Draper,K.G., Dudycz,L.W.,
           Grimm,S., Karpeisky,A., Kisich,K., Matulic-Adamic,J.,
           McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
           Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.B. and
           Woolf,T.
TITLE      Method for purifying chemically modified RNA
JOURNAL    Patent: EP 1502950-A 2740 02-FEB-2005;
           Ribozyme Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
           source
             1..15
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      25 ACTCTGGAGTCCTC 38
Db      14 ACTCTGAAGTCTTC 1

RESULT 79
CS005312
LOCUS      15 bp      DNA      linear      PAT 07-FEB-2005
DEFINITION Sequence 3340 from Patent EPI502950.
ACCESSION CS005312
VERSION    CS005312.1 GI:58740667
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
           unclassified.
REFERENCE  1
AUTHORS    Stinchcomb,D.T., Chowira,B., Direnzo,A., Draper,K.G., Dudycz,L.W.,
           Grimm,S., Karpeisky,A., Kisich,K., Matulic-Adamic,J.,
           McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
           Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.B. and
           Woolf,T.
TITLE      Method for purifying chemically modified RNA
JOURNAL    Patent: EP 1502950-A 3340 02-FEB-2005;
           Ribozyme Pharmaceuticals, Inc. (US)
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               /db_xref="taxon:32644"

Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      29 TGGAGTCCTCTGAG 42
Db      2 TGGAGTACCTTGAG 15

RESULT 80
I39319/c
LOCUS      15 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 357 from patent US 5616488.
ACCESSION I39319
VERSION    I39319.1 GI:2083799
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE      IL-5 targeted ribozymes
JOURNAL    Patent: US 5616488-A 357 01-APR-1997;
           Location/Qualifiers
FEATURES   Location/Qualifiers
           source
             1..15
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Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      25 ACTCTGGAGTCCTC 38
Db      14 ACTCTGAAGTCTTC 1

RESULT 81
I39320/c
LOCUS      15 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 358 from patent US 5616488.
ACCESSION I39320
VERSION    I39320.1 GI:2083800
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE      IL-5 targeted ribozymes
JOURNAL    Patent: US 5616488-A 358 01-APR-1997;
           Location/Qualifiers
FEATURES   Location/Qualifiers
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               /mol_type="unassigned DNA"

Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      25 ACTCTGGAGTCCTC 38
Db      14 ACTCTGAAGTCTTC 1

RESULT 82
I57649/c
LOCUS      15 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 186 from patent US 5610054.
ACCESSION I57649
VERSION    I57649.1 GI:2482713
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Draper,K.G.
TITLE      Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL    Patent: US 5610054-A 186 11-MAR-1997;
           Location/Qualifiers
FEATURES   Location/Qualifiers
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Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGTC 70
Db 15 CCAAGATGATGTC 2

RESULT 83
LOCUS I61819
DEFINITION Sequence 373 from patent US 5658780.
ACCESSION I61819
VERSION I61819.1 GI:2479767
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE Real a targeted ribozymes
JOURNAL Patent: US 5658780-A 373 19-AUG-1997;
FEATURES
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        /mol_type="unassigned DNA"

Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCTCTGAG 42
Db 2 TGGAGTACCTGAG 15

RESULT 84
AX635599/c
LOCUS AX635599
DEFINITION Sequence 2738 from Patent EPI260586.
ACCESSION AX635599
VERSION AX635599.1 GI:28471213
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 2738 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
    source
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        /mol_type="unassigned RNA"
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Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 ACTCTGGAGTCCTC 38
Db 14 ACTCTGAAGTCCTC 1

RESULT 85
AX635601/c
LOCUS AX635601
DEFINITION Sequence 2740 from Patent EPI260586.
ACCESSION AX635601
VERSION AX635601.1 GI:28471215
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 2740 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
    source
        1..15
        /organism="unidentified"
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        /db_xref="taxon:32644"

Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCTCTGAG 42
Db 2 TGGAGTACCTGAG 15

RESULT 87
AR035176
LOCUS AR035176
DEFINITION Sequence 36 from patent US 5871730.

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AX635601/c
LOCUS AX635601
DEFINITION Sequence 2740 from Patent EPI260586.
ACCESSION AX635601
VERSION AX635601.1 GI:28471215
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 2740 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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        /mol_type="unassigned RNA"
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Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 ACTCTGGAGTCCTC 38
Db 14 ACTCTGAAGTCCTC 1

RESULT 86
AX636201
LOCUS AX636201
DEFINITION Sequence 3340 from Patent EPI260586.
ACCESSION AX636201
VERSION AX636201.1 GI:28471815
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 3340 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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        /mol_type="unassigned RNA"
        /db_xref="taxon:32644"

Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCTCTGAG 42
Db 2 TGGAGTACCTGAG 15

RESULT 87
AR035176
LOCUS AR035176
DEFINITION Sequence 36 from patent US 5871730.

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ACCESSION AR035176
VERSION AR035176.1 GI:5951844
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Brzezinski,R., Dery,C.V. and Beaulieu,C.
TITLE Thermostable xylanase DNA, protein and methods of use
JOURNAL Patent: US 5871730-A 36 16-FEB-1999;
FEATURES
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                /mol_type="unassigned DNA"
Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 68;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 56 GCGAAGCTGATG 67
    |||||
Db 2 GCGAGCTGATG 13

RESULT 88
BD263782 13 bp RNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Adeno-associated virus-delivered ribozyme compositions and methods
of use.
ACCESSION BD263782
VERSION BD263782.1 GI:33073550
KEYWORDS JP 2002542805-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 13)
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and
Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods
of use
JOURNAL Patent: JP 2002542805-A 4 17-DEC-2002;
UNIVERSITY OF FLORIDA
COMMENT OS Artificial Sequence
PN JP 2002542805-A/4
PD 17-DEC-2002
PF 28-APR-2000 JP 2000615402
PR 30-APR-1999 US 60/131942
PI ALFRED S LEWIN,NICHOLAS MUZYCZKA,WILLIAM W HAUSWIRTH PI
,CHRISTIAN TESCHENDORF,
PI CORINNA BURGER
PC C12N15/09,A01K67/027,C12N9/00,C12Q1/68,C12N15/00 CC
Description of Artificial Sequence: SYNTHETIC PEPTIDE FH Key
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FEATURES
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        Location/Qualifiers
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                /mol_type="genomic RNA"
                /db_xref="taxon:32630"
Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 68;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTG 40
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Db 1 TGGAGTCCTCTG 12

RESULT 89
AX048268 13 bp RNA linear PAT 15-DEC-2000
LOCUS

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DEFINITION Sequence 4 from Patent WO0066780.
ACCESSION AX048268
VERSION AX048268.1 GI:11877033
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and
Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods
of use
JOURNAL Patent: WO 0066780-A 4 09-NOV-2000;
UNIVERSITY OF FLORIDA (US)
FEATURES
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        Location/Qualifiers
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                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="SYNTHETIC PEPTIDE"
Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 68;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTG 40
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Db 1 TGGAGTCCTCTG 12

RESULT 90
BD209276 14 bp RNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD209276
VERSION BD209276.1 GI:33019046
KEYWORDS JP 2002512791-A/2866.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 2866 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2866
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions
related to
hepatitis C virus infection.
    Location/Qualifiers
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        FT source
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virus)'
                /organism="unidentified"
                /mol_type="genomic RNA"
                /db_xref="taxon:32644"
Query Match 13.5%; Score 10.4; DB 1; Length 14;

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Best Local Similarity 91.7%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 62 CTGATGTCCTGT 73
Db 1 CTGCTGTCCTGT 12

RESULT 91
LOCUS A52274 10 bp DNA linear PAT 12-DEC-1997
DEFINITION Sequence 64 from Patent EP0705842.
ACCESSION A52274
VERSION A52274.1 GI:2852038
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Bartnik,B.D. and Margerie,D.D.
TITLE Regulated genes by stimulation of chondrocytes with 1L-1beta
JOURNAL Patent: EP 0705842-A 64 10-APR-1996;
COMMENT HOECHST AG (DE)
Other publication ZA 9508381 960424
Other publication JP 8191693 960730
Other publication CA 2159957 960407
Other publication AU 3308695 960418.
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 92
LOCUS A91804 10 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 3 from Patent WO9823775.
ACCESSION A91804
VERSION A91804.1 GI:6740684
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Nees,M. and Duerst,M.
TITLE DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
JOURNAL Patent: WO 9823775-A 3 04-JUN-1998;
COMMENT DEUTSCHES KREBSFORSCH (DE); NEES MATTHIAS (DE)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 93
LOCUS A97598 10 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 4 from Patent WO9915680.
ACCESSION A97598
VERSION A97598.1 GI:6780901
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Roberts,J.A. and Paul,W.
TITLE CONTROL OF PLANT ABSCISSION AND POD DEHISCENCE OR SHATTER
JOURNAL Patent: WO 9915680-A 4 01-APR-1999;
COMMENT BIOGENMA UK LIMITED (GB); ROBERTS JEREMY ALAN (GB)
FEATURES
source
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/db_xref="taxon:32644"

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 94
LOCUS AR016246 10 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 14 from patent US 5776683.
ACCESSION AR016246
VERSION AR016246.1 GI:3972523
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Smith,H.S. and Chen,L.-C.
TITLE Methods for identifying genes amplified in cancer cells
JOURNAL Patent: US 5776683-A 14 07-JUL-1998;
FEATURES
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 95
LOCUS AR044027 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5817461.
ACCESSION AR044027
VERSION AR044027.1 GI:5965492
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Austin,R.C., Hirsh,J. and Weitz,J.I.
TITLE Methods and compositions for diagnosis of hyperhomocysteinemia
JOURNAL Patent: US 5817461-A 4 06-OCT-1998;
FEATURES
source
1..10

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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 96
LOCUS AR079092
DEFINITION Sequence 13 from patent US 5965409.
ACCESSION AR079092
VERSION AR079092.1 GI:10005838
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Pardue,A.B. and Liang,P.
TITLE System for comparing levels or amounts of mRNAs
JOURNAL Patent: US 5965409-A 13 12-OCT-1999;
FEATURES
source
Location/Qualifiers
1..10
/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 97
LOCUS AR079528
DEFINITION Sequence 3 from patent US 5965707.
ACCESSION AR079528
VERSION AR079528.1 GI:10006272
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Tam,S.-Y., Tsai,M. and Galli,S.J.
TITLE Rln2, a novel inhibitor of Ras-mediated signaling
JOURNAL Patent: US 5965707-A 3 12-OCT-1999;
FEATURES
source
Location/Qualifiers
1..10
/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 98
LOCUS AR099718
DEFINITION Sequence 28 from patent US 6077948.
ACCESSION AR099718

/organism="unknown"
/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 99
LOCUS AR113051
DEFINITION Sequence 4 from patent US 6132965.
ACCESSION AR113051
VERSION AR113051.1 GI:14093373
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Austin,R.C., Hirsh,J. and Weitz,J.I.
TITLE Methods and compositions for diagnosis of hyperhomocysteinemia
JOURNAL Patent: US 6132965-A 4 17-OCT-2000;
FEATURES
source
Location/Qualifiers
1..10
/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 100
LOCUS BD107610
DEFINITION Novel microsatellite DNA derived from pear plants and method for discriminating pear plants using the same.
ACCESSION BD107610
VERSION BD107610.1 GI:23202428
KEYWORDS JP 2002034597-A/19.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Yamamoto,T., Sawamura,Y., Imai,T., Matsuda,N., Saito,T., Shoda,M.,
Kotobuki,K., Hayashi,K., Ba,Y., Kozono,M. and Kimura,T.
TITLE Novel microsatellite DNA derived from pear plants and method for discriminating pear plants using the same
JOURNAL Patent: JP 2002034597-A 19 05-FEB-2002;
COMMENT FRUIT TREE RES STATION
OS Artificial Sequence
FN JP 2002034597-A/19
PD 05-FEB-2002

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PF 21-JUL-2000 JP 2000220339
PI TOSHIYA YAMAMOTO,TUTAKA SAWAMURA,TSUYOSHI IMAI,NAGAO MATSUDA,
PI TOSHIHIRO SAITO,MORIYUKI SHODA,KAZUO KOTOBUKI,KENKI HAYASHI,
PI YOSHIYUKI BAN,
PI MASANORI KOZONO,TETSUYA KIMURA
PC C12N1/69,A01H1/00,C12N15/09,C12N15/00
CC Description of Artificial Sequence:Primer
FH Key Location/Qualifiers
FT source
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/organism='Artificial Sequence'.
FEATURES
source
1. .10
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10
|||||
1 AGCCAGCGAA 10

RESULT 101
BD240697
LOCUS BD240697 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240697
VERSION BD240697.1 GI:33050467
KEYWORDS JP 2002534056-A/2115.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 2115 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/2115
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089977,19-JUN-1998 US 60/090079 PR
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19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
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19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,GRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K35/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source
1. .10
/organism='Homo sapiens (human)'.
FEATURES
source
1. .10
Location/Qualifiers

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/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 ACAAGACGGC 13
Db 1 ACAAGACGGC 10
|||||
1 ACAAGACGGC 10

RESULT 102
BD248338
LOCUS BD248338 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Tobacco-origin novel salicylic acid-inducible gene and promoter.
ACCESSION BD248338
VERSION BD248338.1 GI:33058108
KEYWORDS JP 2002524051-A/14.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 10)
AUTHORS Stuijver,M.H., Jepson,I., Horvath,D.M. and Chua,N.H.
TITLE Tobacco-origin novel salicylic acid-inducible gene and promoter
JOURNAL Patent: JP 2002524051-A 14 06-AUG-2002;
SYNGENTA MOGEN BV
COMMENT OS Artificial Sequence
PN JP 2002524051-A/14
PD 06-AUG-2002
PF 02-AUG-1999 JP 2000563809
PR 03-AUG-1998 US 60/095187
PI MAARTEN HENDRIK STUIJVER,IAN JEPSON,DIANA MEREDITH HORVATH,NAM
PI HAI CHUA
PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC
Description of Artificial Sequence Primer API FH Key
Location/Qualifiers
FT source
1. .10
/organism='Artificial Sequence'.
FEATURES
source
1. .10
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10
|||||
1 AGCCAGCGAA 10

RESULT 103
LOCUS I22447
DEFINITION Sequence 28 from patent US 5527884.
ACCESSION I22447
VERSION I22447.1 GI:1602801
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Russell,M.S. and Utans,U.
TITLE Mediators of chronic allograft rejection and DNA molecules encoding them
JOURNAL Patent: US 5527884-A 28 18-JUN-1996;
FEATURES
source
1. .10
Location/Qualifiers
/organism='unknown'

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/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      51 AGCCAGCGAA 60
Db      1 AGCCAGCGAA 10
        |||||
        |||||

RESULT 104
LOCUS      I34793
DEFINITION Sequence 13 from patent US 5599672.
ACCESSION  I34793
VERSION    I34793.1 GI:2087761
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Liang,P.; Pardee,A.B. and Bianchi,C.F.
TITLE     Method of differential display of exposed mRNA by RT/PCR
JOURNAL   Patent: US 5599672-A 13 04-FEB-1997;
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      51 AGCCAGCGAA 60
Db      1 AGCCAGCGAA 10
        |||||
        |||||

RESULT 105
LOCUS      I64511
DEFINITION Sequence 13 from patent US 5665547.
ACCESSION  I64511
VERSION    I64511.1 GI:2481405
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Pardee,A.B. and Liang,P.
TITLE     Methods of comparing levels or amounts of mRNAs
JOURNAL   Patent: US 5665547-A 13 09-SEP-1997;
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      51 AGCCAGCGAA 60
Db      1 AGCCAGCGAA 10
        |||||
        |||||

RESULT 106
LOCUS      AR238724
DEFINITION Sequence 132 from patent US 6468743.
ACCESSION  AR238724
VERSION    AR238724.1 GI:27283794

/mol_type="unassigned DNA"

KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Romick,T.L. and Fraser,M.S.
TITLE     PCR techniques for detecting microbial contaminants in foodstuffs
JOURNAL   Patent: US 6468743-A 132 22-OCT-2002;
          ConAgra Grocery Products Company; Fullerton, CA
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      51 AGCCAGCGAA 60
Db      1 AGCCAGCGAA 10
        |||||
        |||||

RESULT 107
LOCUS      AR270938
DEFINITION Sequence 3 from patent US 6500942.
ACCESSION  AR270938
VERSION    AR270938.1 GI:29702188
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Tam,S.-Y., Tsai,M. and Galli,S.J.
TITLE     Rin2, a novel inhibitor of Ras-mediated signaling
JOURNAL   Patent: US 6500942-A 3 31-DEC-2002;
          Beth Israel Deaconess Medical Center and The Board of Trustees of
          the Leland Stanford, Jr., University; Palo Alto, CA
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      51 AGCCAGCGAA 60
Db      1 AGCCAGCGAA 10
        |||||
        |||||

RESULT 108
LOCUS      AX016299
DEFINITION Sequence 2 from Patent WO949046.
ACCESSION  AX016299
VERSION    AX016299.1 GI:10041862
KEYWORDS   .
SOURCE     synthetic construct
          other sequences; artificial sequences.
ORGANISM   1
REFERENCE  1
AUTHORS   Roberts,J.A., Wyatt,P. and Whitelaw,C.
TITLE     Signal transduction protein involved in plant dehiscence
JOURNAL   Patent: WO 9949046-A 2 30-SEP-1999;
          ROBERTS JEREMY ALAN (GB); BIOEMMA UK LTD (GB); WYATT PAUL (GB);
          WHITELAW CATHERINE (GB)
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
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/db_xref="taxon:32630"
/notes="Arbitrary primer A"

Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
   |||||
Db 1 AGCCAGCGAA 10

RESULT 109
AX152307/c
LOCUS AX152307 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 222 from Patent WO0138577.
ACCESSION AX152307
VERSION AX152307.1 GI:14533958
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Velculescu,V.B., Vogelstein,B. and Kinzler,K.W.
Human transcriptomes
TITLE Patent: WO 0138577-A 222 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGGCGTCGGG 19
   |||||
Db 10 CGGCGTCGGG 1

RESULT 110
BD023238
LOCUS BD023238 10 bp DNA linear PAT 27-AUG-2002
DEFINITION DNA for evaluating progress potential of cervical diseases.
ACCESSION BD023238
VERSION BD023238.1 GI:22564461
KEYWORDS JP 2001504703-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
Durst,M. and Ness,M.
DNA for evaluating progress potential of cervical diseases
TITLE Patent: JP 2001504703-A 3 10-APR-2001;
JOURNAL DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES EFFENTLICHEN RECHTS
COMMENT PN JP 2001504703-A/3
PD 10-APR-2001
PF 12-NOV-1997 JP 1998524127
PR 27-NOV-1996 DE 19649207.6
PI MATHIAS DURST,MATHIAS NESS
PC C12N15/09,C07K14/00,C07K16/00,C12P21/02,C12Q1/68,C12Q1/70, PC
G01N33/574,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'Primer'
FH Key Location/Qualifiers.

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FEATURES
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1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
   |||||
Db 1 AGCCAGCGAA 10

RESULT 111
AR641426
LOCUS AR641426 13 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 14 from patent US 6861057.
ACCESSION AR641426
VERSION AR641426.1 GI:62776633
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 13)
Gaudernack,G., Eriksen,J.A. and Moller,M.
Immunogenic .beta.-amyloid peptide
TITLE Patent: US 6861057-A 14 01-MAR-2005;
JOURNAL GenVex AS; Oslo;
NOX;
FEATURES
source
1. .13
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 TCTGAGAGGT 46
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Db 1 TCTGAGAGGT 10

RESULT 112
AR051174/c
LOCUS AR051174 14 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5830654.
ACCESSION AR051174
VERSION AR051174.1 GI:5974538
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 14)
Milliman,C.L.
TITLE Nucleic acid probes to Haemophilus influenzae
JOURNAL Patent: US 5830654-A 2 03-NOV-1998;
FEATURES
source
1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 AGCGAGAGCTG 64
   |||||
Db 12 AGCGAGAGCTG 3

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RESULT 113
BD068997/c
LOCUS
DEFINITION
Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION
BD068997
VERSION
BD068997.1 GI:22614600
KEYWORDS
JP 2001511003-A/1837.
SOURCE
unidentified
ORGANISM
unclassified.
1 (bases 1 to 14)
REFERENCE
AUTHORS
Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE
Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors
JOURNAL
Patent: JP 2001511003-A 1837 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT
OS Unidentified
PN JP 2001511003-A/1837
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
CC levels of epidermal growth factor receptors
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Unidentified'.
FEATURES
source
1..14
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 AGAGCCAGCG 58
|||||
DB 14 AGAGCCAGCG 5
RESULT 114
BD197865/c
LOCUS
DEFINITION
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION
BD197865
VERSION
BD197865.1 GI:33007635
KEYWORDS
JP 2002509721-A/891.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 14)
REFERENCE
AUTHORS
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL
Patent: JP 2002509721-A 891 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Homo sapiens (human)
PN JP 2002509721-A/891
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN

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PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..14
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 58 GAAGCTGATG 67
|||||
DB 10 GAAGCTGATG 1
RESULT 115
I15960/c
LOCUS
DEFINITION
Sequence 2 from patent US 5472843.
ACCESSION
I15960
VERSION
I15960.1 GI:1250868
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Milliman,C.L.
TITLE
Nucleic acid probes to Haemophilus influenzae
JOURNAL
Patent: US 5472843-A 2 05-DEC-1995;
FEATURES
Location/Qualifiers
source
1..14
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 55 AGCGAAGCTG 64
|||||
DB 12 AGCGAAGCTG 3
RESULT 116
AR403497/c
LOCUS
DEFINITION
Sequence 1837 from patent US 6623962.
ACCESSION
AR403497
VERSION
AR403497.1 GI:40150947
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE
Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
JOURNAL
Patent: US 6623962-A 1837 23-SEP-2003;
SIRNA THERAPEUTICS, INC. and ASTON UNIVERSITY; BOULDER, CO
FEATURES
Location/Qualifiers
source
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/organism="unknown"

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/mol_type="genomic DNA"

Query Match      13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 AGAGCCAGCG 58
    |||||
Db 14 AGAGCCAGCG 5

RESULT 117
LOCUS AR069833 13 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 49 from patent US 5891685.
ACCESSION AR069833
VERSION AR069833.1 GI:7220721
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Yamagishi,M., Takai,Y., Mikawa,T., Hara,M., Ueda,M. and Ohara,A.
TITLE (S)- gamma -halogenated- beta -hydroxybutyric acid
JOURNAL Patent: US 5891685-A 49 08-APR-1999;
FEATURES Location/Qualifiers
    source
        1..13
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 60 AGCTGATGTCCTG 72
    |||||
Db 13 AGCTGATGACTTG 1

RESULT 118
LOCUS E15186/c 13 bp DNA linear PAT 28-JUL-1999
DEFINITION Selenophoma donacis CBS417.51 - specific sequence in 16S rRNA gene.
ACCESSION E15186
VERSION E15186.1 GI:5709869
KEYWORDS JP 1998052290-A/19.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 13)
AUTHORS Yamagishi,M., Takai,Y., Mikawa,T., Oohara,A., Hara,M. and Ueda,M.
TITLE PRODUCTION OF (S)-GAMMA-HALOGENATED-BETA-HYDROXYLACTIC ACID ESTER
JOURNAL Patent: JP 1998052290-A 19 24-FEB-1998;
COMMENT MITSUBISHI CHEM CORP
OS Selenophoma donacis
PN JP 1998052290-A/19
PD 24-FEB-1998
PF 03-JUN-1997 JP 1997145613
PR 03-JUN-1996 JP 96P 140087
PI YAMAGISHI MASAHIRO, TAKAI YUKIE, MIKAWA TAKASHI, OOHARA AKIKO,
PI HARA MARI,
PI UEDA MAKOTO
PC C12P7/62, (C12P7/62,C12R1:645) ;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..13
    /organism='Selenophoma donacis' FT
    /strain='CBS417.51',
    Location/Qualifiers
    1..13

/mol_type="genomic DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 64 GATGTCTCTGTCAC 76
    |||||
Db 13 GATGTACTGCCAA 1

RESULT 120
LOCUS AR196782/c 13 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1247 from patent US 6350934.
ACCESSION AR196782
VERSION AR196782.1 GI:20246219
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Zwick,M.G., Edgington,B.E., McSwiggen,J.A., Merlo,P,Ann Owens.,
Gao,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 1247 26-FEB-2002;
FEATURES Location/Qualifiers
    source
        1..13
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 26 CTCTGGAGTCCTC 38
    |||||
Db 13 CTCTAGAGTCCCC 1

RESULT 121
LOCUS AR027402/c 14 bp DNA linear PAT 29-SEP-1999
DEFINITION
ACCESSION AR027402
VERSION AR027402.1
KEYWORDS
SOURCE

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DEFINITION Sequence 62 from patent US 5856188.
ACCESSION AR027402
VERSION AR027402.1 GI:5938222
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Hampel,A.E., Tritz,R.H. and Hicks,M.F.
TITLE Hairpin ribozymes
JOURNAL Patent: US 5856188-A 62 05-JAN-1999;
FEATURES
    source
        1..14
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAACAGACGGCC 14
Db 14 AAACAGACGGTC 2

RESULT 122
AR028856/c
LOCUS AR028856
DEFINITION Sequence 62 from patent US 585785.
ACCESSION AR028856
VERSION AR028856.1 GI:5940829
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Hampel,A.E. and Tritz,R.H.
TITLE HIV targeted ribozymes
JOURNAL Patent: US 585785-A 62 12-JAN-1999;
FEATURES
    source
        1..14
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAACAGACGGCC 14
Db 14 AAACAGACGGTC 2

RESULT 123
AR034393/c
LOCUS AR034393
DEFINITION Sequence 62 from patent US 5869339.
ACCESSION AR034393
VERSION AR034393.1 GI:5949998
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Hampel,A.E., Tritz,R.H. and Hicks,M.F.
TITLE HIV targeted hairpin ribozymes
JOURNAL Patent: US 5869339-A 62 09-FEB-1999;
FEATURES
    source
        1..14
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAACAGACGGCC 14
Db 14 AAACAGACGGTC 2

RESULT 124
AR043142/c
LOCUS AR043142
DEFINITION Sequence 26 from patent US 5814453.
ACCESSION AR043142
VERSION AR043142.1 GI:5964150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Beck,J.Joseph.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5814453-A 26 29-SEP-1998;
FEATURES
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        1..14
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGGGG 19
Db 13 AGACGGCCTCCGG 1

RESULT 125
AR074642/c
LOCUS AR074642
DEFINITION Sequence 26 from patent US 5955274.
ACCESSION AR074642
VERSION AR074642.1 GI:10001395
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Ligon,J.M. and Beck,J.J.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5955274-A 26 21-SEP-1999;
FEATURES
    source
        1..14
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGGGG 19
Db 13 AGACGGCCTCCGG 1

RESULT 126
AR082205/c
LOCUS AR082205
DEFINITION Sequence 49 from patent US 5972704.
ACCESSION AR082205
VERSION AR082205.1 GI:10008931
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
TITLE HIV nef targeted ribozymes
JOURNAL Patent: US 5972704-A 49 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..14
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Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCT 71
Db 14 AAGCTGGTGTTCT 2

RESULT 127
AR120747/c
LOCUS AR120747 14 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 49 from patent US 6159692.
ACCESSION AR120747
VERSION AR120747.1 GI:14104323
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
TITLE Method and reagent for inhibiting human immunodeficiency virus replication
JOURNAL Patent: US 6159692-A 49 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..14
/mol_type="unassigned DNA"

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCT 71
Db 14 AAGCTGGTGTTCT 2

RESULT 128
AR164788
LOCUS AR164788 14 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 99 from patent US 6274332.
ACCESSION AR164788
VERSION AR164788.1 GI:16237972
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE Mutations in the KCNE1 gene encoding human minK which cause arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL Patent: US 6274332-A 99 14-AUG-2001;
FEATURES Location/Qualifiers
source 1..14
/mol_type="unassigned DNA"

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14

RESULT 129
BD068929
LOCUS BD068929 14 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.
ACCESSION BD068929
VERSION BD068929.1 GI:22614532
KEYWORDS JP 2001511003-A/1769.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 1769 07-AUG-2001;
COMMENT RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
PN JP 2001511003-A/1769
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PT
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC related to
CC levels of epidermal growth factor receptors
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Unidentified'.

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GACGGCCTGGGA 20
Db 2 GACGGCGGGGCA 14

RESULT 130
BD209346
LOCUS BD209346 14 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD209346
VERSION BD209346.1 GI:33019116
KEYWORDS JP 2002512791-A/2936.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 2936 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2936
PD 08-MAY-2002

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PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
FVACO, DENNIS MACEJAK
PI C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC C12N37/66,
PC A61K37/66,
PC C12N15/00,
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..14
/organism="Hepatitis virus (hepatitis C FT
virus)"
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source
Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GACGGCTGGGGA 20
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DB 2 GACGGCTGGGGA 14

RESULT 131
LOCUS BD222899 14 bp DNA linear PAT 17-JUL-2003
DEFINITION KVLQ1-QT extension syndrome.
ACCESSION BD222899
VERSION BD222899.1 GI:33032669
KEYWORDS JP 2002521045-A/97,
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 14)
AUTHORS Keating,M.T., Sanguinetti,M.C., Karan,M.E., Landes,G.M.,
Connors,T.D., Burn,T.C. and Splawski,I.
TITLE KVLQ1-QT extension syndrome
JOURNAL Patent: JP 2002521045-A 97 16-JUL-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION,GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002521045-A/97
PD 16-JUL-2002
PP 12-MAY-1999 JP 2000562052
PR 29-JUL-1998 US 60/094477,17-AUG-1998 US 09/135010 PI
MARK T KEATING,MICHAEL C SANGUINETTI,MARK E KARAN,GREGORY M PI
LANDES.
PI TIMOTHY D CONNORS,TIMOTHY C BURN,IGOR SPLAWSKI PC
C12N15/09,A01K67/027,C07K14/46,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/08,C12Q1/02,C12Q1/68,G01N33/15,G01N33/ PC
50, G01N33/53,G01N33/53,G01N33/566,G01N33/577,G01N33/58,G01N33/68,
PC C12N15/00,
PC C12N5/00
CC KVLQ1-QT extension syndrome
FH Key Location/Qualifiers
FT source 1..14
/organism="Homo sapiens (human)"
/organism="Homo sapiens"
/mol_type="genomic DNA"

FEATURES
source
Location/Qualifiers
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Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 TCCTCTGAGAGGT 46
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DB 2 TCCTTTAAGAGGT 14

RESULT 132
LOCUS I32082 14 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 26 from patent US 5585238.
ACCESSION I32082
VERSION I32082.1 GI:1822873
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Ligon,J.M. and Beck,J.J.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5585238-A 26 17-DEC-1996;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCTGGGG 19
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DB 13 AGACGGCTCCGG 1

RESULT 133
LOCUS I78251 14 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 49 from patent US 5693535.
ACCESSION I78251
VERSION I78251.1 GI:3014405
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and
Thompson,J.D.
TITLE HIV targeted ribozymes
JOURNAL Patent: US 5693535-A 49 02-DEC-1997;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AGCTGATGTCCT 71
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DB 14 AGCTGGTGTCT 2

RESULT 134
LOCUS AR179956 14 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 24 from patent US 633152.
ACCESSION AR179956

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VERSION      AR179956.1  GI:20221989
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE        Gene expression profiles in normal and cancer cells
JOURNAL      Patent: US 633152-A 24 25-DEC-2001;
FEATURES     Location/Qualifiers
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             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 65 ATGTCCTGTCAG 77
Db 2 ATGTCCTATTAG 14

RESULT 135
AR218751
LOCUS      AR218751          14 bp      DNA          linear      PAT 25-SEP-2002
DEFINITION Sequence 99 from patent US 6420124.
ACCESSION  AR218751
VERSION     AR218751.1  GI:23319646
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
              Connors,T.D., Burn,T.C. and Splawski,I.
TITLE        KVLQT1--a long qt syndrome gene
JOURNAL      Patent: US 6420124-A 99 16-JUL-2002;
              University of Utah Research Foundation and Genzyme Corporation;
              Salt Lake City, UT
FEATURES     Location/Qualifiers
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             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14

RESULT 136
AR223166
LOCUS      AR223166          14 bp      DNA          linear      PAT 26-SEP-2002
DEFINITION Sequence 99 from patent US 6432644.
ACCESSION  AR223166
VERSION     AR223166.1  GI:23331019
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE        Mutations in the KCNE1 gene encoding human minK which cause
              arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL      Patent: US 6432644-A 99 13-AUG-2002;
              University of Utah Research Foundation; Salt Lake City, UT
FEATURES     Location/Qualifiers
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Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14

RESULT 137
AR229928
LOCUS      AR229928          14 bp      DNA          linear      PAT 20-DEC-2002
DEFINITION Sequence 99 from patent US 6451534.
ACCESSION  AR229928
VERSION     AR229928.1  GI:27269806
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
              Connors,T.D., Burn,T.C. and Splawski,I.
TITLE        KVLQT1--a long QT syndrome gene
JOURNAL      Patent: US 6451534-A 99 17-SEP-2002;
              University of Utah Research Foundation and Genzyme Corporation;
              Salt Lake City, UT
FEATURES     Location/Qualifiers
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             /mol_type="genomic DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14

RESULT 138
AR262184
LOCUS      AR262184          14 bp      DNA          linear      PAT 29-JAN-2003
DEFINITION Sequence 99 from patent US 6323026.
ACCESSION  AR262184
VERSION     AR262184.1  GI:28073545
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE        Mutations in the KCNE1 gene encoding human minK which cause
              arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL      Patent: US 6323026-A 99 27-NOV-2001;
              University of Utah Research Foundation; Salt Lake City, UT
FEATURES     Location/Qualifiers
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             /organism="unknown"
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Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14

RESULT 139
AR262184
LOCUS      AR262184          14 bp      DNA          linear      PAT 29-JAN-2003
DEFINITION Sequence 99 from patent US 6323026.
ACCESSION  AR262184
VERSION     AR262184.1  GI:28073545
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE        Mutations in the KCNE1 gene encoding human minK which cause
              arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL      Patent: US 6323026-A 99 27-NOV-2001;
              University of Utah Research Foundation; Salt Lake City, UT
FEATURES     Location/Qualifiers
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Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14

RESULT 139

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AR344622
LOCUS AR344622 14 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 99 from patent US 6582913.
ACCESSION AR344622
VERSION AR344622.1 GI:33740691
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 14)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
Conners,T.D., Burn,T.C. and Splawski,I.
TITLE Diagnostic method for KVLQTL1--a long QT syndrome gene
JOURNAL Patent: US 6582913-A 99 24-JUN-2003;
University of Utah Research Foundation and Genzyme, Inc.; Salt Lake
City, UT
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Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14
RESULT 140
AR403429
LOCUS AR403429 14 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1769 from patent US 6623962.
ACCESSION AR403429
VERSION AR403429.1 GI:40150879
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 14)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: US 6623962-A 1769 23-SEP-2003;
Sirna Therapeutics, Inc. and Aston University; Boulder, CO
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Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 GACGGCGTGGGA 20
Db 2 GACGGCGGGGCA 14
RESULT 141
AX467015/c
LOCUS AX467015 14 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 44 from Patent WO224950.
ACCESSION AX467015
VERSION AX467015.1 GI:21900356
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
AUTHORS Liang,Z., Zhang,H.Y. and Wahlestedt,C.
TITLE Methods and means of rna analysis

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JOURNAL Patent: WO 0224950-A 44 28-MAR-2002;
Neuromics Inc. (US)
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/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetically generated oligonucleotide"
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 61 GCTGATGTCCTCT 73
Db 13 GCTGATGTCCTCT 1
RESULT 142
AX710784/c
LOCUS AX710784 14 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 84 from Patent EP1288296.
ACCESSION AX710784
VERSION AX710784.1 GI:29787165
KEYWORDS
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
REFERENCE
1
AUTHORS Draper,K.G., McSwiggen,J.A., Holecek,J.J., Dudycz,L.W.,
Macejak,D.G. and Mamone,J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 84 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
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Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 59 AGCTGATGTCCT 71
Db 14 AGCTGGTGTCT 2
RESULT 143
BD000925/c
LOCUS BD000925 14 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD000925
VERSION BD000925.1 GI:18625484
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 (bases 1 to 14)
AUTHORS Draper,K.G., Dadykztz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342285-A 85 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Artificial Sequence
PN JP 2000342285-A/85
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132616
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR

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14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
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26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22// (C12N5/10, C12R1:91), PC
C12N15/00,
PC C12N5/00, (C12N5/00, C12R1:91)
CC
FH Key Location/Qualifiers
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/organism='Artificial Sequence'.
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/mol_type='genomic RNA'
/db_xref='taxon:32630'
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 59 AAGCTGATGTCCT 71
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DB 14 AAGCTGGTGTCT 2

RESULT 144
BD001354/c
LOCUS
DEFINITION
Method and reagent for inhibiting viral replication.
ACCESSION
BD001354
VERSION
JP 2000342286-A/85.
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
1 (bases 1 to 14)
REFERENCE
1 Draper, K.G., Dadyktz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holesek, J.J. and Mamone, A.J.
TITLE
Method and reagent for inhibiting viral replication
JOURNAL
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Artificial Sequence
PN JP 2000342286-A/85
PD 12-DEC-2000
PF 01-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
PR 11-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
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14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
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14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR
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14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
26-AUG-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
31-JUL-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK, ANTHONY J MAMONE

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PC C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,
PC A61K39/135,
PC A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
PC A61P1/16,
PC A61P31/14, A61P31/16, A61P31/18, A61P31/22, A61P35/02, C12O1/68, PC
(C12N15/09, C12R1:93), C12N15/00, C12N5/00, A61K37/48, (C12N15/00, PC
C12R1:93)
CC
FH Key Location/Qualifiers
FT source 1..14
/organism='Artificial Sequence'.
FEATURES
source
1..14
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 59 AAGCTGATGTCCT 71
||||| |||||
DB 14 AAGCTGGTGTCT 2

RESULT 145
S81872S11/c
LOCUS
DEFINITION
Gogo-DRB8=MHC-DRB pseudogene [Gorilla gorilla=western lowland
gorilla, ssp. gorilla, Genomic, 14 nt, segment 11 of 12].
ACCESSION
S81875
VERSION
S81875.1 GI:244229
KEYWORDS
11 of 12
SEGMENT
Gorilla gorilla (gorilla)
SOURCE
Gorilla gorilla
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Gorilla.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Klein, D., Vincsek, V., Kasahara, M., Schonbach, C., O'huigin, C. and
Klein, J.
TITLE
Gorilla major histocompatibility complex-DRB pseudogene orthologous
to HLA-DRBVIII
JOURNAL
Hum. Immunol. 32 (3), 211-220 (1991)
PUBMED
1774200
REMARK
GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 81875] from the original journal article.
FEATURES
source
1..14
Location/Qualifiers
/organism='Gorilla gorilla'
/mol_type='genomic DNA'
/db_xref='taxon:9593'
join(S81872.1:6..285,S81873.1:1..111,S81874.1:1..24,1..14)
/genes='Gogo-DRB8'
/notes='MHC-DRB pseudogene'
/pseudo
/codon_start=1
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 23 CAAGCTCGAGTC 35
||||| |||||
DB 13 CAGCTCAGGAGTC 1

RESULT 146
A57558/c
LOCUS
DEFINITION
Sequence 50 from Patent WO9632483.
A57558
11 bp DNA linear PAT 03-MAR-1998

```

```

ACCESSION A57558
VERSION A57558.1 GI:3713392
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Masucci,M.G.
TITLE IMMUNE-EVADING PROTEINS
JOURNAL Patent: WO 9632483-A 50 17-OCT-1996;
COMMENT MASUCCI MARIA GRAZIA (SE)
Other publication AU 5284296 961030.
FEATURES
    source
        1. .11
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 GGGGATACAC 26
Db 11 GGGGATCCAC 1
RESULT 147
AR030142
LOCUS AR030142 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 331 from patent US 5861244.
ACCESSION AR030142
VERSION AR030142.1 GI:5943356
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 331 19-JAN-1999;
FEATURES
    source
        1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 40 GAGAGGTAAAG 50
Db 1 GAGAGGGAAG 11
RESULT 148
CQ835708
LOCUS CQ835708 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 766 from Patent WO2004059001.
ACCESSION CQ835708
VERSION CQ835708.1 GI:50835242
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
CONRADT,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 766 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
QY 54 CAGCGAAGCTG 64
Db 11 CAGCAAGCTG 1
Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 54 CAGCGAAGCTG 64
Db 11 CAGCAAGCTG 1
RESULT 150
CQ836081/c
LOCUS CQ836081/c 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1139 from Patent WO2004059001.
ACCESSION CQ836081
VERSION CQ836081.1 GI:50835615
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
CONRADT,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 1139 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
QY 54 CAGCGAAGCTG 64
Db 11 CAGCAAGCTG 1
Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 54 CAGCGAAGCTG 64
Db 11 CAGCAAGCTG 1
RESULT 150
CQ836081/c
LOCUS CQ836081/c 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1139 from Patent WO2004059001.
ACCESSION CQ836081
VERSION CQ836081.1 GI:50835615
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
CONRADT,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 1139 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
QY 54 CAGCGAAGCTG 64
Db 11 CAGCAAGCTG 1
Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 54 CAGCGAAGCTG 64
Db 11 CAGCAAGCTG 1

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Best Local Similarity 90.9%; Pred. No. 88;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 62 CTGATGTCCTG 72  
Db 11 CTGATGTCCTG 1

RESULT 151

LOCUS CQ836100 11 bp DNA linear PAT 29-JUL-2004

DEFINITION Sequence 1158 from Patent WO2004059001.

ACCESSION CQ836100

VERSION CQ836100.1 GI:50835634

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1

AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,

CONRADT,M. and Hofmann,K.

TITLE Method for determining markers of human facial skin

JOURNAL Patent: WO 2004059001-A 1158 15-JUL-2004;

FEATURES Henkel Kommanditgesellschaft auf Aktien (DB)

Location/Qualifiers

1. .11

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

source

Query Match 12.2%; Score 9.4; DB 1; Length 11;

Best Local Similarity 90.9%; Pred. No. 88;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAAGAGGCCT 15

Db 11 CAAGAGGCCT 1

RESULT 152

LOCUS CQ837567 11 bp DNA linear PAT 29-JUL-2004

DEFINITION Sequence 2625 from Patent WO2004059001.

ACCESSION CQ837567

VERSION CQ837567.1 GI:50837101

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1

AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,

CONRADT,M. and Hofmann,K.

TITLE Method for determining markers of human facial skin

JOURNAL Patent: WO 2004059001-A 2625 15-JUL-2004;

FEATURES Henkel Kommanditgesellschaft auf Aktien (DB)

Location/Qualifiers

1. .11

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

source

Query Match 12.2%; Score 9.4; DB 1; Length 11;

Best Local Similarity 90.9%; Pred. No. 88;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGATACACTC 28

Db 1 GGATACACAC 11

RESULT 153

LOCUS CS021382 11 bp DNA linear PAT 23-FEB-2005

DEFINITION Sequence 814 from Patent WO2005012576.

ACCESSION CS021382

VERSION CS021382.1 GI:60221937

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Sebastian,S.

TITLE Molecular markers for the selection of soybean plants having

JOURNAL superior agronomic performance

Patent: WO 2005012576-A 814 10-FEB-2005;

FEATURES Pioneer Hi-Bred International Inc. (US)

Location/Qualifiers

1. .11

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/notes="oligonucleotide probe"

source

Query Match 12.2%; Score 9.4; DB 1; Length 11;

Best Local Similarity 90.9%; Pred. No. 88;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 AGAGCCAGCGA 59

Db 1 AGAGCCAGTGA 11

RESULT 154

LOCUS CS058360 11 bp DNA linear PAT 13-APR-2005

DEFINITION Sequence 257 from Patent WO2005028671.

ACCESSION CS058360

VERSION CS058360.1 GI:62551543

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1

AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and

Kessler-Becker,D.

TITLE Method for determining hair cycle markers

JOURNAL Patent: WO 2005028671-A 257 31-MAR-2005;

FEATURES Henkel Kommanditgesellschaft auf Aktien (DB)

Location/Qualifiers

1. .11

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

source

Query Match 12.2%; Score 9.4; DB 1; Length 11;

Best Local Similarity 90.9%; Pred. No. 88;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 AAGAGCCAGCG 58

Db 1 AAGAGCCAGCG 11

RESULT 155

LOCUS CS058436 11 bp DNA linear PAT 13-APR-2005

DEFINITION Sequence 333 from Patent WO2005028671.

ACCESSION CS058436

VERSION CS058436.1 GI:62551619

KEYWORDS

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
            Kessler-Becker,D.
TITLE       Method for determining hair cycle markers
JOURNAL     Patent: WO 2005028671-A 333 31-MAR-2005;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      48 AAGAGCCAGCG 58
Db      1 AAGAACCAGCG 11

RESULT 156
LOCUS     CS058451              11 bp      DNA      linear      PAT 13-APR-2005
DEFINITION Sequence 348 from Patent WO2005028671.
ACCESSION CS058451
VERSION   CS058451.1 GI:62551634
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
            Kessler-Becker,D.
TITLE       Method for determining hair cycle markers
JOURNAL     Patent: WO 2005028671-A 348 31-MAR-2005;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 GGCCTGGGGAT 21
Db      1 GGCCTGGGGAT 11

RESULT 157
LOCUS     CS058533              11 bp      DNA      linear      PAT 13-APR-2005
DEFINITION Sequence 430 from Patent WO2005028671.
ACCESSION CS058533
VERSION   CS058533.1 GI:62551716
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
            Kessler-Becker,D.
TITLE       Method for determining hair cycle markers
JOURNAL     Patent: WO 2005028671-A 430 31-MAR-2005;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      54 CACGAGAGCTG 64
Db      11 CAGCAAGCTG 1

RESULT 159
LOCUS     AX627490              11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4531 from Patent WO20053774.
ACCESSION AX627490
VERSION   AX627490.1 GI:28455528
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4531 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      54 CACGAGAGCTG 64
Db      11 CAGCAAGCTG 1

```

Query Match 12.2%; Score 9.4; DB 1; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 88;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GGCCTGGGGAT 21  
 |||||  
 Db 1 GGCCTGGGGT 11

## RESULT 160

AX628152 AX628152 11 bp DNA linear PAT 21-FEB-2003  
 LOCUS Sequence 5193 from Patent WO02053774.  
 DEFINITION AX628152  
 ACCESSION AX628152  
 VERSION AX628152.1 GI:28456190

KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

## REFERENCE

1 Petersohn,D., Conradt,M. and Hofmann,K.  
 AUTHORS Method for determining homeostasis of the skin  
 TITLES  
 JOURNAL Patent: WO 02053774-A 5193 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)

## FEATURES

source  
 1..11  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 12.2%; Score 9.4; DB 1; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 88;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGATACAACTC 28  
 |||||  
 Db 1 GGATACAAAC 11

## RESULT 161

AX630121 AX630121 11 bp DNA linear PAT 21-FEB-2003  
 LOCUS Sequence 7162 from Patent WO02053774.  
 DEFINITION AX630121  
 ACCESSION AX630121  
 VERSION AX630121.1 GI:28458159

KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

## REFERENCE

1 Petersohn,D., Conradt,M. and Hofmann,K.  
 AUTHORS Method for determining homeostasis of the skin  
 TITLES  
 JOURNAL Patent: WO 02053774-A 7162 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)

## FEATURES

source  
 1..11  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 12.2%; Score 9.4; DB 1; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 88;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 56 GCGAAGCTGAT 66  
 |||||  
 Db 1 GTGAAGCTGAT 11

## RESULT 162

BD240909/c BD240909 12 bp DNA linear PAT 17-JUL-2003  
 LOCUS Expression and export of angiogenesis inhibitors as immunofusins.  
 DEFINITION BD240909

ACCESSION BD240909  
 VERSION BD240909.1 GI:33050679  
 KEYWORDS JP 2002523036-A/29.  
 SOURCE synthetic construct

## ORGANISM

synthetic construct  
 other sequences; artificial sequences.

## REFERENCE

1 (bases 1 to 12)  
 Lo,K.M., Li,Y. and Gillies,S.D.

AUTHORS Expression and export of angiogenesis inhibitors as immunofusins  
 TITLES  
 JOURNAL Patent: JP 2002523036-A 29 30-JUL-2002;  
 LEXIGEN PHARMACEUTICALS CORP

## COMMENT

OS Artificial Sequence  
 PN JP 2002523036-A/29  
 PD 30-JUL-2002

PF 25-AUG-1999 JP 2000566305  
 PR 25-AUG-1998 US 60/097883  
 PI KIN MING LO,YUE LI,STEPHEN D GILLIES

PC C12N15/09,A61K31/711,A61K38/00,A61K39/395,A61K48/00,A61P7/00,  
 A61P35/00  
 PC A61P43/00,C07K14/745,C07K19/00,C12N5/10,C12P21/02,  
 C12N15/00,  
 PC C12N5/00,A61K37/02

CC Description of Artificial Sequence: BamHI/HindIII CC linker:  
 top strand  
 FH Key Location/Qualifiers  
 FT CDS (3)..(11).

## FEATURES

source  
 1..12  
 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

Query Match 12.2%; Score 9.4; DB 1; Length 12;  
 Best Local Similarity 90.9%; Pred. No. 93;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GGCCTGGGGAT 21  
 |||||  
 Db 12 GGCCTGGGGAT 2

## RESULT 163

CQ766172/c CQ766172 12 bp DNA linear PAT 03-MAR-2004  
 LOCUS Sequence 133 from Patent WO2004005547.  
 DEFINITION CQ766172  
 ACCESSION CQ766172  
 VERSION CQ766172.1 GI:44908432

KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

## REFERENCE

1 Weinzierl,R.

AUTHORS

TITLE

JOURNAL

Patent: WO 2004005547-A 133 15-JAN-2004;  
 IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)

## FEATURES

source  
 1..12  
 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="HS consensus sequence"

Query Match 12.2%; Score 9.4; DB 1; Length 12;  
 Best Local Similarity 90.9%; Pred. No. 93;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 62 CTGATGCTCTG 72

```

Db      11 CAGATGCTCTG 1
      | |||||
RESULT 164
LOCUS   CQ766282/c
DEFINITION Sequence 243 from Patent WO2004005547.
ACCESSION CQ766282
VERSION   CQ766282.1 GI:44908542
KEYWORDS .
SOURCE   synthetic construct
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Hashiguchi,K., Nakai,Y. and Itou,H.
TITLE    Method for producing l-amino acid by fermentation
JOURNAL  Patent: WO 2005049808-A 8 02-JUN-2005;
          Ajinomoto Co., Inc. (JP)
FEATURES Location/Qualifiers
          source
            1..12
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Description of Artificial Sequence : XbaI linker
              for linkage to thrA and a ttenuator"

Query Match 12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      58 GAAGCTGATGT 68
Db      12 GAAGCTGTTGT 2

RESULT 165
LOCUS   CS104143
DEFINITION Sequence 8 from Patent WO2005049808.
ACCESSION CS104143
VERSION   CS104143.1 GI:67512417
KEYWORDS .
SOURCE   synthetic construct
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Hashiguchi,K., Nakai,Y. and Itou,H.
TITLE    Method for producing l-amino acid by fermentation
JOURNAL  Patent: WO 2005049808-A 8 02-JUN-2005;
          Ajinomoto Co., Inc. (JP)
FEATURES Location/Qualifiers
          source
            1..12
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Description of Artificial Sequence : XbaI linker
              for linkage to thrA and a ttenuator"

Query Match 12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      25 ACTCTGGAGTC 35
Db      2 ACTCTAGAGTC 12

RESULT 166
LOCUS   CS104143/c
DEFINITION Sequence 8 from Patent WO2005049808.
ACCESSION CS104143
VERSION   CS104143.1 GI:67512417

```

```

KEYWORDS .
SOURCE   synthetic construct
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Hashiguchi,K., Nakai,Y. and Itou,H.
TITLE    Method for producing l-amino acid by fermentation
JOURNAL  Patent: WO 2005049808-A 8 02-JUN-2005;
          Ajinomoto Co., Inc. (JP)
FEATURES Location/Qualifiers
          source
            1..12
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Description of Artificial Sequence : XbaI linker
              for linkage to thrA and a ttenuator"

Query Match 12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      25 ACTCTGGAGTC 35
Db      11 ACTCTAGAGTC 1

RESULT 167
LOCUS   AR475028
DEFINITION Sequence 415 from patent US 6692917.
ACCESSION AR475028
VERSION   AR475028.1 GI:42714165
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
          Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Neri,B.P., Hall,J.G., Lyamichiev,V. and Smith,L.M.
TITLE    Systems and methods for invasive cleavage reaction on dendrimers
JOURNAL  Patent: US 6692917-A 415 17-FEB-2004;
          Third Wave Technologies, INC; Madison, WI
FEATURES Location/Qualifiers
          source
            1..12
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      31 GAGTCCTCTGA 41
Db      1 GAGTCCTCTGA 11

RESULT 168
LOCUS   AX097978
DEFINITION Sequence 46 from Patent WO0118048.
ACCESSION AX097978
VERSION   AX097978.1 GI:13514757
KEYWORDS .
SOURCE   synthetic construct
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS van Eijs,G.J., Hateboer,G. and Havenga,M.J.
TITLE    Smooth muscle cell promoter and uses thereof
JOURNAL  Patent: WO 0118048-A 46 15-MAR-2001;
          Introgene B.V. (NL)
FEATURES Location/Qualifiers
          source
            1..12
              /organism="synthetic construct"

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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="variant intron-exon splice recognition sequences"

Query Match 12.2%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 93;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 40 GAGAGGTAAG 50  
|||||  
Db 2 GAGAGGTAGAG 12

## RESULT 169

AX138554  
LOCUS AX138554 12 bp DNA linear PAT 30-MAY-2001  
DEFINITION Sequence 46 from Patent EP1083231.  
ACCESSION AX138554  
VERSION AX138554.1 GI:14274449

KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS  
TITLE Smooth muscle cell promoter and uses thereof  
JOURNAL Introgene B.V. (NL)  
FEATURES  
source Location/Qualifiers  
1. .12  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="variant intron-exon splice recognition sequences"

Query Match 12.2%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 93;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 40 GAGAGGTAAG 50  
|||||  
Db 2 GAGAGGTAGAG 12

RESULT 170  
AX772212/c  
LOCUS AX772212 12 bp DNA linear PAT 02-JUL-2003  
DEFINITION Sequence 2 from Patent WO03042407.  
ACCESSION AX772212  
VERSION AX772212.1 GI:32438785

KEYWORDS  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster

REFERENCE 1  
AUTHORS Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
TITLE Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
JOURNAL Ephydroidea; Drosophilidae; Drosophila.  
FEATURES  
source Location/Qualifiers  
1. .12  
/organism="Drosophila melanogaster"  
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/db\_xref="taxon:7227"

Qy 40 GAGAGGTAAG 50  
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Db 2 GAGAGGTAGAG 12

RESULT 171  
AX772212/c  
LOCUS AX772212 12 bp DNA linear PAT 02-JUL-2003  
DEFINITION Sequence 2 from Patent WO03042407.  
ACCESSION AX772212  
VERSION AX772212.1 GI:32438785

KEYWORDS  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster

REFERENCE 1  
AUTHORS Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
TITLE Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
JOURNAL Ephydroidea; Drosophilidae; Drosophila.  
FEATURES  
source Location/Qualifiers  
1. .12  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:7227"

Qy 40 GAGAGGTAAG 50  
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Db 2 GAGAGGTAGAG 12

RESULT 172  
AX772212/c  
LOCUS AX772212 12 bp DNA linear PAT 02-JUL-2003  
DEFINITION Sequence 2 from Patent WO03042407.  
ACCESSION AX772212  
VERSION AX772212.1 GI:32438785

KEYWORDS  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster

REFERENCE 1  
AUTHORS Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
TITLE Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
JOURNAL Ephydroidea; Drosophilidae; Drosophila.  
FEATURES  
source Location/Qualifiers  
1. .12  
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Qy 40 GAGAGGTAAG 50  
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Db 2 GAGAGGTAGAG 12

RESULT 173  
AX772212/c  
LOCUS AX772212 12 bp DNA linear PAT 02-JUL-2003  
DEFINITION Sequence 2 from Patent WO03042407.  
ACCESSION AX772212  
VERSION AX772212.1 GI:32438785

KEYWORDS  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster

REFERENCE 1  
AUTHORS Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
TITLE Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
JOURNAL Ephydroidea; Drosophilidae; Drosophila.  
FEATURES  
source Location/Qualifiers  
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/organism="Drosophila melanogaster"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:7227"

Qy 40 GAGAGGTAAG 50  
|||||  
Db 2 GAGAGGTAGAG 12

RESULT 174  
AX772212/c  
LOCUS AX772212 12 bp DNA linear PAT 02-JUL-2003  
DEFINITION Sequence 2 from Patent WO03042407.  
ACCESSION AX772212  
VERSION AX772212.1 GI:32438785

KEYWORDS  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster

Db 12 CTGATGTCCTG 2  
|||||

## RESULT 171

AR019451  
LOCUS AR019451 13 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 39 from patent US 5783431.  
ACCESSION AR019451  
VERSION AR019451.1 GI:3974565

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Peterson,T.C., Foster,L.M. and Brian,P.

TITLE Methods for generating and screening novel metabolic pathways  
JOURNAL Patent: US 5783431-A 39 21-JUL-1998;  
FEATURES  
source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAA 60  
|||||  
Db 3 GAGCCAGCTAA 13

RESULT 172  
AR029150/c  
LOCUS AR029150 13 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 26 from patent US 5859221.  
ACCESSION AR029150  
VERSION AR029150.1 GI:5941123

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Cook,P.Dan. and Kawasaki,A.Mamoru.

TITLE 2'-modified oligonucleotides  
JOURNAL Patent: US 5859221-A 26 12-JAN-1999;  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAA 60  
|||||  
Db 3 GAGCCAGCTAA 13

RESULT 173  
AR036534/c  
LOCUS AR036534 13 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 26 from patent US 5972232.  
ACCESSION AR036534  
VERSION AR036534.1 GI:5953202

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Cook,P.Dan. and Kawasaki,A.Mamoru.

TITLE 2'-O-modified oligonucleotides  
JOURNAL Patent: US 5972232-A 26 12-JAN-1999;  
FEATURES  
source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGG 17  
|||||  
Db 12 AAACGGCCTGG 2

RESULT 174  
AR036534/c  
LOCUS AR036534 13 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 26 from patent US 5972232.  
ACCESSION AR036534  
VERSION AR036534.1 GI:5953202

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Cook,P.Dan. and Kawasaki,A.Mamoru.

TITLE 2'-O-modified oligonucleotides  
JOURNAL Patent: US 5972232-A 26 12-JAN-1999;  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGG 17  
|||||  
Db 12 AAACGGCCTGG 2

RESULT 175  
AR036534/c  
LOCUS AR036534 13 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 26 from patent US 5972232.  
ACCESSION AR036534  
VERSION AR036534.1 GI:5953202

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Cook,P.Dan. and Kawasaki,A.Mamoru.

TITLE 2'-O-modified oligonucleotides  
JOURNAL Patent: US 5972232-A 26 12-JAN-1999;  
FEATURES  
source Location/Qualifiers  
1. .13  
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/mol\_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 93;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 62 CTGATGTCCTG 72  
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RESULT 176  
AR036534/c  
LOCUS AR036534 13 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 26 from patent US 5972232.  
ACCESSION AR036534  
VERSION AR036534.1 GI:5953202

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Cook,P.Dan. and Kawasaki,A.Mamoru.

TITLE 2'-O-modified oligonucleotides  
JOURNAL Patent: US 5972232-A 26 12-JAN-1999;  
FEATURES  
source Location/Qualifiers  
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JOURNAL Patent: US 5872232-A 26 16-FEB-1999;  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGACGGCCTGG 17  
| | | | | | | | | |  
Db 12 AAACGGCCTGG 2

RESULT 174  
LOCUS AR096067/c 13 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 26 from patent US 6005087.  
ACCESSION AR096067  
VERSION AR096067.1 GI:10024532  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Cook, P. Dan. and Kawasaki, A. Mamoru.  
TITLE 2'-modified oligonucleotides  
JOURNAL Patent: US 6005087-A 26 21-DEC-1999;  
FEATURES  
source  
1. .13  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGACGGCCTGG 17  
| | | | | | | | | |  
Db 12 AAACGGCCTGG 2

RESULT 175  
LOCUS AR156401 13 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 30 from patent US 6242211.  
ACCESSION AR156401  
VERSION AR156401.1 GI:15125105  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Peterson, T. C. and Brian, P.  
TITLE Methods for generating and screening novel metabolic pathways  
JOURNAL Patent: US 6242211-A 30 05-JUN-2001;  
FEATURES  
source  
1. .13  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAA 60  
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Db 3 GAGCCAGCTAA 13

RESULT 176  
LOCUS AR174824/c 13 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 26 from patent US 639754.  
ACCESSION AR212300  
VERSION AR212300.1 GI:21515837  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Cook, P. Dan.  
TITLE Sugar modified oligonucleotides

LOCUS AR174824 13 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 6 from patent US 6307040.  
ACCESSION AR174824  
VERSION AR174824.1 GI:17915144  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Cook, P. Dan. and Kawasaki, A. M.  
TITLE Sugar modified oligonucleotides that detect and modulate gene expression  
JOURNAL Patent: US 6307040-A 6 23-OCT-2001;  
FEATURES  
source  
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/organism="unknown"  
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Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGACGGCCTGG 17  
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Db 12 AAACGGCCTGG 2

RESULT 177  
LOCUS CQ828552 13 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 270 from Patent WO2004053120.  
ACCESSION CQ828552  
VERSION CQ828552.1 GI:49732035  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Rattus.

REFERENCE 1  
AUTHORS Weihe, E., Bieller, A. and Schaefer, M. K.  
TITLE Regulatory elements in the 5' region of the vrl gene  
JOURNAL Patent: WO 2004053120-A 270 24-JUN-2004;  
FEATURES  
source  
1. .13  
/organism="Rattus norvegicus"  
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/db\_xref="taxon:10116"  
/note="V\$GATA1 04"

Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 62 CTGATGTCCTG 72  
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Db 3 CTGATATCTG 13

RESULT 178  
LOCUS AR212300/c 13 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 26 from patent US 639754.  
ACCESSION AR212300  
VERSION AR212300.1 GI:21515837  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Cook, P. Dan.  
TITLE Sugar modified oligonucleotides

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JOURNAL Patent: US 6399754-A 26 04-JUN-2002;
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Query Match      12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AGAGGCGCTGG 17
Db 12 AAAGCGCTGG 2

RESULT 179
AR285769
LOCUS      13 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 141 from patent US 6528640.
ACCESSION AR285769
VERSION AR285769.1 GI:29723363
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpelsky,A.,
TITLE Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
JOURNAL Synthetic ribonucleic acids with RNase activity
PATENT: US 6528640-A 141 04-MAR-2003;
Ribozyne Pharmaceuticals, Inc.; Boulder, CO
FEATURES Location/Qualifiers
  source
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Query Match      12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGC 57
Db 2 AGAGGCGCAGC 12

RESULT 180
AR397760
LOCUS      13 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 141 from patent US 6617438.
ACCESSION AR397760
VERSION AR397760.1 GI:40135004
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpelsky,A.,
TITLE Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
JOURNAL Oligoribonucleotides with enzymatic activity
PATENT: US 6617438-A 141 09-SEP-2003;
Sirna Therapeutics, Inc.; Boulder, CO
FEATURES Location/Qualifiers
  source
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Query Match      12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGC 57
Db 2 AGAGGCGCAGC 12

JOURNAL Patent: US 6399754-A 26 04-JUN-2002;
FEATURES Location/Qualifiers
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Query Match      12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AGAGGCGCTGG 17
Db 12 AAAGCGCTGG 2

RESULT 181
AR658253/c
LOCUS      13 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 8 from patent US 6897025.
ACCESSION AR658253
VERSION AR658253.1 GI:67592186
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Cox,D.R., Margus,B.A. and Patil,N.
TITLE Genetic analysis systems and methods
JOURNAL Patent: US 6897025-A 8 24-MAY-2005;
Perlegen Sciences, Inc.; Mountain View, CA
FEATURES Location/Qualifiers
  source
    1. .13
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      /mol_type="genomic DNA"

Query Match      12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TAAAGAGCCAG 56
Db 12 TAAAGAGTCAG 2

RESULT 182
AX813993
LOCUS      13 bp DNA linear PAT 02-DEC-2003
DEFINITION Sequence 5 from Patent EPI316605.
ACCESSION AX813993
VERSION AX813993.1 GI:38636318
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Aotsuka,S.
TITLE Method for producing DNA
JOURNAL Patent: EP 1316605-A 5 04-JUN-2003;
NITSHINBO INDUSTRIES, INC. (JP)
FEATURES Location/Qualifiers
  source
    1. .13
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      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="synthetic DNA"
  misc_feature
    7
      /note="n=a, g, t or c"

Query Match      12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 28 CTGGAGTCCTCT 39
Db 1 CTGGAGNCGTCT 12

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Job time : 0.001 secs

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GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM nucleic - nucleic search, using sw model  
 Run on: April 19, 2006, 16:04:57 ; Search time 0.001 Seconds  
 (without alignments)  
 12.936 Million cell updates/sec

Title: US-10-643-038-17\_994-1070  
 Perfect score: 77  
 Sequence: 1 caacaagagcgctgggga.....gaagctgatctctgtcaag 77

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 84 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 8 summaries

Database : estdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Length	DB ID	Description
C 1	9	11.7	11 1	ACCESSION:AJ651054
C 2	8.4	10.9	11 1	ACCESSION:AJ590125
C 3	8.4	10.9	11 1	ACCESSION:CL983148
4	7.8	10.1	11 1	ACCESSION:BQ111753
5	7.4	9.6	10 1	ACCESSION:BQ789997
6	7.4	9.6	10 1	ACCESSION:CL659790
7	7.4	9.6	10 1	ACCESSION:CL686823
8	7.4	9.6	10 1	ACCESSION:CT007455

## ALIGNMENTS

RESULT 1  
 LOCUS AJ651054/c  
 DEFINITION AJ651054 CSEQRAN19 Sus scrofa cDNA clone C0003277\_B19, mRNA  
 11 bp mRNA linear EST 07-JUL-2004  
 sequence.  
 ACCESSION AJ651054  
 VERSION AJ651054.1 GI:49327899  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.  
 REFERENCE 1 (bases 1 to 11)  
 AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
 TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Anderson SI  
 Genomics and Bioinformatics

Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13p Normalised library constructed from pooled ovaries. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.ark-genomics.org.  
 Location/Qualifiers

## FEATURES

source

1. .11  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
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 /clone\_lib="CSEQRAN19"  
 /notes="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing; Normalised library constructed from pooled ovaries"

Query Match 11.7%; Score 9; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4 ACAAGACGG 12  
 |||||  
 Db 9 ACAAGACGG 1

## RESULT 2

AJ590125/c

LOCUS

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence, left border, clone

563G02, genomic survey sequence.

ACCESSION

AJ590125

VERSION

AJ590125.1 GI:37939749

KEYWORDS

GSS; left border; T-DNA flanking sequence.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS

Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,

Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,

Lepiniec,L., Caboche,M. and Lecharny,A.

T-DNA integration into the Arabidopsis genome depends on sequences

of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

PUBMED

12446565

REFERENCE

2 (bases 1 to 11)

AUTHORS

Balzergue,S.

TITLE

Direct Submission

JOURNAL

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (http://www.genoplante.com and

http://genoplante-info.infobiofr.fr).

## FEATURES

source

1. .11  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="563G02"

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misc_feature      /clone lib="Arabidopsis thaliana T-DNA insertion lines"
                  1. .11
                  /ecotype="Wassilewskija"
                  /notes="T-DNA flanking sequence
                  left border"

Query Match      10.9%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 42 GAGTAAGA 51
Db 11 GAGTAAGA 2

RESULT 3
CL983148/c
LOCUS
DEFINITION      GC0387 TIGEM gene trap library Mus musculus cDNA clone A012.B10,
                  mRNA sequence.
ACCESSION      CL983148
VERSION        CL983148.1 GI:52420779
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 11)
                Cobellis,G., Nicolaus,G., Iovino,M., Romito,A., Marra,E.,
                Barbarisi,M., Sardiello,M., Di Giorgio,F.P., Iovino,N., Zollo,M.,
                Ballabio,A. and Cortese,R.
                Tagging genes with cassette-exchange sites
                Nucleic Acids Res. 33 (4), e44 (2005)
JOURNAL        15741177
PUBMED
COMMENT        Contact: TIGEM
                107
                TIGEM
                Via P. Castellino, 111, 80131 NAPOLI, ITALY
                Tel: +390816132205
                Fax: +390815790919
                Email: cobellis@tigem.it
                Sequence tag generated by 5' RACE of total RNA from gene trap ES
                cell line. ES cell lines harboring insertion mutation of target
                gene are available upon request from TIGEM. Annotation information
                available from TIGEM
                Class: Gene Trap.
FEATURES
source
Location/Qualifiers
1. .11
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/clone="A012.B10"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/notes="vector: pFLIP1"

Query Match      10.9%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGAGTCCT 37
Db 11 CTGGGTCCT 2

RESULT 4
BQ111753
LOCUS
DEFINITION      EST597329 mixed potato tissues Solanum tuberosum cDNA clone STMCC84

misc_feature      /clone lib="Arabidopsis thaliana T-DNA insertion lines"
                  1. .11
                  /ecotype="Wassilewskija"
                  /notes="T-DNA flanking sequence
                  left border"

Query Match      10.9%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 42 GAGTAAGA 51
Db 11 GAGTAAGA 2

RESULT 3
CL983148/c
LOCUS
DEFINITION      GC0387 TIGEM gene trap library Mus musculus cDNA clone A012.B10,
                  mRNA sequence.
ACCESSION      CL983148
VERSION        CL983148.1 GI:52420779
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 11)
                Cobellis,G., Nicolaus,G., Iovino,M., Romito,A., Marra,E.,
                Barbarisi,M., Sardiello,M., Di Giorgio,F.P., Iovino,N., Zollo,M.,
                Ballabio,A. and Cortese,R.
                Tagging genes with cassette-exchange sites
                Nucleic Acids Res. 33 (4), e44 (2005)
JOURNAL        15741177
PUBMED
COMMENT        Contact: TIGEM
                107
                TIGEM
                Via P. Castellino, 111, 80131 NAPOLI, ITALY
                Tel: +390816132205
                Fax: +390815790919
                Email: cobellis@tigem.it
                Sequence tag generated by 5' RACE of total RNA from gene trap ES
                cell line. ES cell lines harboring insertion mutation of target
                gene are available upon request from TIGEM. Annotation information
                available from TIGEM
                Class: Gene Trap.
FEATURES
source
Location/Qualifiers
1. .11
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/clone="A012.B10"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/notes="vector: pFLIP1"

Query Match      10.9%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGAGTCCT 37
Db 11 CTGGGTCCT 2

RESULT 4
BQ111753
LOCUS
DEFINITION      EST597329 mixed potato tissues Solanum tuberosum cDNA clone STMCC84

```

```

5' end, mRNA sequence.
BQ111753
VERSION          BQ111753.1 GI:20163715
KEYWORDS
SOURCE           Solanum tuberosum (potato)
ORGANISM         Solanum tuberosum
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE        1 (bases 1 to 11)
                Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
                Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
                Karamycheva,S.A.
                Generation of a set of potato cDNA clones for microarray analyses
                Unpublished (2002)
JOURNAL
COMMENT          Contact: Robin Buell
                The Institute for Genomic Research
                9712 Medical Center Dr, Rockville, MD 20850, USA
                Email: potato-array@tigr.org
                This clone can be obtained from the University of Arizona Genomics
                Institute. Orders can be made through URL:
                http://genome.arizona.edu/orders/
                Seq primer: T3.
FEATURES
source
Location/Qualifiers
1. .11
/mol_type="mRNA"
/cultivar="Kennebec or Binjite"
/db_xref="taxon:4113"
/clone="STMCC84"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/clone_lib="mixed potato tissues"
/notes="Vector: pBluescript SK(-), Site 1: EcoRI; Site 2:
                XhoI; supplier: Combination of untreated and Phytophthora
                infestans-treated libraries of stolons, leaves, leaflets,
                axillary buds of stem explants, petioles, germinating
                eyes, tubers, or roots."

Query Match      10.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 45 GTAAAGAGCCA 55
Db 1 GGAAGGCCA 11

RESULT 5
BQ789997
LOCUS
DEFINITION      BQ789997 10 bp mRNA linear EST 30-JUL-2002
                hage005ad02 Heterobasidion annosum - Scots pine infection stage
                (HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion
                annosum mixed EST library cDNA clone hage005ad02, mRNA sequence.
ACCESSION      BQ789997
VERSION        BQ789997.1 GI:22004959
KEYWORDS       EST.
SOURCE         Pinus sylvestris/Heterobasidion annosum mixed EST library
                Eukaryota; mixed EST libraries.
ORGANISM       Pinus sylvestris/Heterobasidion annosum mixed EST library
                Eukaryota; mixed EST libraries.
REFERENCE      1 (bases 1 to 10)
                Asiegbu,P.O., Nahalkova,J. and Dean,R.A.
                Selected Expressed sequence tags of cDNA clones from the
                interaction of the root rot fungus (Heterobasidion annosum) with
                seedling roots of Scots pine (Pinus sylvestris)
                Unpublished (2001)
JOURNAL
COMMENT          Contact: Fred O. Asiegbu
                Dept. of Forest Mycology & Pathology
                Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                Sweden
                Tel: +46 18 67 15 98
                Fax: +46 18 30 92 45
                Email: Fred.Asiegbu@mykopat.slu.se

```

```

FEATURES
  source
    Seq primer: T7 primer.
    Location/Qualifiers
      1..10
        EST library"
        /organism="Pinus sylvestris/Heterobasidion annosum mixed
        /mol_type="mRNA"
        /db_xref="taxon:169015"
        /clone="hage005ab02"
        /dev_stage="Seedling roots of scots pine were infected for
        6 days with H. annosum"
        /clone_lib="Heterobasidion cDNA library"
        /stage (HAGE) subtraction cDNA library"
        /note="vector: pT-Adv; Site 1: EcoRI; The subtractive
        hybridization cDNA library was constructed from scots pine
        roots infected for 6-days with mycelia of Heterobasidion
        annosum (FP5)."
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Query Match 9.6%; Score 7.4; DB 1; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 3.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 36 CTCGTGAG 44  
 |||||  
 Db 1 CTCGTATAG 9

```

RESULT 6
LOCUS
  CL659790
  DEFINITION
    CL659790 B11 - PRI0135b.B21 (10) Mixed stage fosmid library of P.
    pacificus var. California Pristionchus pacificus genomic, genomic
    survey sequence.
  ACCESSION
    CL659790
  VERSION
    CL659790.1 GI:50144248
  KEYWORDS
    GSS.
  SOURCE
    Pristionchus pacificus
    Pristionchus pacificus
    Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
    Neodiplogasteridae; Pristionchus.
  REFERENCE
    1 (bases 1 to 10)
    Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
    AppADB: an Acedb database for the nematode satellite organism
    Pristionchus pacificus
    Nucleic Acids Res. 32 (1), D421-D422 (2004)
  JOURNAL
    PUBLISHED
    COMMENT
      Contact: Sommer RJ
      Evolutionary Biology
      Max-Planck-Institute for Developmental Biology
      Spemannstr. 37-39, Tuebingen D-72076, Germany
      Tel: 00497071601371
      Fax: 00497071601498
      Email: ralf.sommer@tuebingen.mpg.de
      This library was generated at Caltech, Pasadena, USA and end
      sequenced at Vancouver, Canada.
      Seq primer: T7
      Class: fosmid ends.
      Location/Qualifiers
        1..10
          /organism="Pristionchus pacificus"
          /mol_type="genomic DNA"
          /strain="California"
          /db_xref="taxon:54126"
          /clone_lib="Mixed stage fosmid library of P. pacificus
          var. California"
          /note="Vector: pBifos-5 Fosmid vector"
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Query Match 9.6%; Score 7.4; DB 1; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 3.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 44 GGTAAAGAG 52  
 |||||  
 Db 10 GATTAAGAG 2

```

RESULT 8
LOCUS
  T7115122
  DEFINITION
    T7115122 Equus caballus GSS, BAC clone CH241-115122, T7 end sequence,
    genomic survey sequence.
  ACCESSION
    CT007455
  VERSION
    CT007455.1 GI:67967256
  KEYWORDS
    GSS; genomic survey sequence.
  SOURCE
    Equus caballus (horse)
    Equus caballus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
  REFERENCE
    1 (bases 1 to 10)
    Leeb,T., Binns,M.M., de Jong,P.J., Berg,C., Conrad,A., Jarek,M.,
    Loehner,T.H., Nordisiek,G., Severitt,S., Scharfe,S.,
    Schindewolf,C., Schrader,F., Thies,S. and Bloecker,H.
    Analysis of horse BAC sequences
    Unpublished
    2 (bases 1 to 10)
    Jarek,M.
    Direct Submission
    TITLE
    JOURNAL
    AUTHORS
    TITLE
    JOURNAL
```

Query Match 9.6%; Score 7.4; DB 1; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 3.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 CCTGGGGAT 21  
 |||||  
 Db 1 CCGGGGAT 9

```

RESULT 7
LOCUS
  CL686823/c
  DEFINITION
    CL686823 A03.2 - PRI0145b.BR (10) Mixed stage fosmid library of P.
    pacificus var. California Pristionchus pacificus genomic, genomic
    survey sequence.
  ACCESSION
    CL686823
  VERSION
    CL686823.1 GI:50195421
  KEYWORDS
    GSS.
  SOURCE
    Pristionchus pacificus
    Pristionchus pacificus
    Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
    Neodiplogasteridae; Pristionchus.
  REFERENCE
    1 (bases 1 to 10)
    Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
    AppADB: an Acedb database for the nematode satellite organism
    Pristionchus pacificus
    Nucleic Acids Res. 32 (1), D421-D422 (2004)
  JOURNAL
    PUBLISHED
    COMMENT
      Contact: Sommer RJ
      Evolutionary Biology
      Max-Planck-Institute for Developmental Biology
      Spemannstr. 37-39, Tuebingen D-72076, Germany
      Tel: 00497071601371
      Fax: 00497071601498
      Email: ralf.sommer@tuebingen.mpg.de
      This library was generated at Caltech, Pasadena, USA and end
      sequenced at Vancouver, Canada.
      Seq primer: T7
      Class: fosmid ends.
      Location/Qualifiers
        1..10
          /organism="Pristionchus pacificus"
          /mol_type="genomic DNA"
          /strain="California"
          /db_xref="taxon:54126"
          /clone_lib="Mixed stage fosmid library of P. pacificus
          var. California"
          /note="Vector: pBifos-5 Fosmid vector"
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Query Match 9.6%; Score 7.4; DB 1; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 3.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 44 GGTAAAGAG 52  
 |||||  
 Db 10 GATTAAGAG 2

```

RESULT 8
LOCUS
  T7115122
  DEFINITION
    T7115122 Equus caballus GSS, BAC clone CH241-115122, T7 end sequence,
    genomic survey sequence.
  ACCESSION
    CT007455
  VERSION
    CT007455.1 GI:67967256
  KEYWORDS
    GSS; genomic survey sequence.
  SOURCE
    Equus caballus (horse)
    Equus caballus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
  REFERENCE
    1 (bases 1 to 10)
    Leeb,T., Binns,M.M., de Jong,P.J., Berg,C., Conrad,A., Jarek,M.,
    Loehner,T.H., Nordisiek,G., Severitt,S., Scharfe,S.,
    Schindewolf,C., Schrader,F., Thies,S. and Bloecker,H.
    Analysis of horse BAC sequences
    Unpublished
    2 (bases 1 to 10)
    Jarek,M.
    Direct Submission
    TITLE
    JOURNAL
    AUTHORS
    TITLE
    JOURNAL
```

Query Match 9.6%; Score 7.4; DB 1; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 3.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 CCTGGGGAT 21  
 |||||  
 Db 1 CCGGGGAT 9

for Biotechnology, Mascheroder Weg 1, Braunschweig D-38124, Germany

FEATURES

source

1. .10  
/organism="Equus caballus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9796"  
/clone="CH241-115122"  
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/note="sequenced with T7 primer"

Query Match

Best Local Similarity 9.6%; Score 7.4; DB 1; Length 10;

Matches 8; Conservativity 88.9%; Pred.No.3.8;

Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 ATCAACTC 28

|||||

Db 2 ATACGACTC 10

Search completed: April 19, 2006, 16:04:57

Job time : 0.001 secs

XX This oligonucleotide can hybridize to nucleic acids encoding  
CC phospholipase A2 typical of the synovial fluid of patients with  
CC rheumatoid arthritis. (SF-PLA2 is more closely related to group II PLA2  
CC enzymes such as those in rattlesnake venom than to pancreatic PLA2). The  
CC oligonucleotide (especially its phosphorothioate analogue) would be  
CC useful in inhibiting SF-PLA2 expression. SF-PLA2 secretion has been  
CC detected from a human epidermal carcinoma cell line and primary human  
CC epidermal keratinocytes. This suggests that the inhibitory  
CC oligonucleotide would be useful in the treatment of inflammatory  
CC disorders of the skin. See AAQ14859-Q14895  
XX  
SQ Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;  
  
Query Match 27.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.9;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 20 ATACAACTCTGGAGTCTCTG 40  
Db 21 ATACAACTCTGGAGTCTCTG 1  
  
RESULT 3  
AAQ61918/c  
ID AAQ61918 standard; DNA; 21 BP.  
XX  
AC AAQ61918;  
XX  
DT 25-MAR-2003 (revised)  
DT 04-NOV-1994 (first entry)  
XX  
DE Human type II phospholipase A2 inhibiting oligomer, ISIS no 3182.  
XX  
KW Inhibition; replication; herpes simplex virus; HSV; HIV; aging;  
KW human cytomegalovirus; influenza virus; inflammation; telomere length;  
KW neurological disorders; phospholipase A2 activity; hyperproliferation;  
KW malignancy; cardiovascular disease; snake bite; malignancy; retard; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1..21  
FT /\*tag= a  
FT /note= "Phosphorothioate intersugar linkages"  
XX  
PN W09408053-A1.  
XX  
PD 14-APR-1994.  
XX  
PF 29-SEP-1993; 93WO-US009297.  
XX  
PR 29-SEP-1992; 92US-00954185.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
PI Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;  
PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;  
XX  
DR WPI; 1994-135613/16.  
XX  
PT New modified oligo-nucleotide contg guanine quartet - inhibits activity  
PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length  
PT of chromosomes.  
XX  
PS Disclosure; Page 26; 144pp; English.  
XX  
CC The sequences given in AAQ61917-55 are oligonucleotides which contain a  
CC G4 stretch and which may be used for inhibiting phospholipase A2 enzyme  
CC activity. Oligonucleotides such as these may also be used for inhibiting  
CC activity of HSV, HIV, human cytomegalovirus or influenza virus, or for  
CC treating inflammatory and neurological disorders caused by phospholipase  
CC A2 activity in cases of hyperproliferation, malignancy, cardiovascular

CC disease and snake bite. They may also be used for inhibiting division of  
CC malignant cells by modulating telomere length, which may also retard  
CC aging. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;  
  
Query Match 27.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.9;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 20 ATACAACTCTGGAGTCTCTG 40  
Db 21 ATACAACTCTGGAGTCTCTG 1  
  
RESULT 4  
ACC46928/c  
ID ACC46928 standard; DNA; 20 BP.  
XX  
AC ACC46928;  
XX  
DT 05-JUN-2003 (first entry)  
XX  
DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:25.  
XX  
KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;  
KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;  
KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;  
KW psoriasis; diabetes; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate backbone"  
FT modified\_base 1..5  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"  
XX  
PN WQ200297133-A1.  
XX  
PD 05-DEC-2002.  
XX  
PF 21-MAY-2002; 2002WO-US016135.  
XX  
PR 25-MAY-2001; 2001US-00865866.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
PI Bennett CF, Wyatt JR;  
XX  
DR WPI; 2003-140495/13.  
XX  
PT New compound that hybridizes with and inhibits the expression of  
PT phospholipase A2, group IIA, useful for preparing a composition for  
PT treating or preventing inflammation, cancer, psoriasis or diabetes.  
XX  
PS Claim 3; Page 86; 135pp; English.  
XX  
CC The present invention describes a compound (I) comprising 8-50  
CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,  
CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase  
CC A2, group IIA (synovial), where the compound specifically hybridizes with  
CC and inhibits the expression of phospholipase A2, group IIA (synovial).  
CC Also described: (1) a composition comprising the compound and a carrier





GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 16:12:08 ; Search time 0.001 Seconds  
(without alignments)  
677.446 Million cell updates/sec

Title: US-10-643-038-17\_994-1070

Perfect score: 77

Sequence: 1 caaacaagacggctgggga.....gaagctgatgtcctgtcaag 77

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 292 seqs, 4399 residues

Total number of hits satisfying chosen parameters: 584

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 299 summaries

Database : ngsdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	28.2	36.6	33	1	AAQ26374
C 2	21	27.3	21	1	AAQ14886
C 3	21	27.3	21	1	AAQ61918
C 4	20	26.0	20	1	ACC46928
C 5	20	26.0	20	1	ACC46927
C 6	20	26.0	20	1	ACC46926
C 7	20	26.0	20	1	ACC46925
C 8	20	26.0	20	1	ACC46922
C 9	20	26.0	20	1	ACC46924
C 10	20	26.0	20	1	ACC46923
C 11	17.8	23.1	21	1	ACL45000
C 12	16.8	21.8	21	1	ACL44998
C 13	16.8	21.8	21	1	ACL44994
C 14	16.8	21.8	21	1	ACL44996
C 15	16.4	21.3	21	1	ACL44495
C 16	16.4	21.3	21	1	ACL44497
C 17	16.4	21.3	21	1	ACL44499
C 18	16.4	21.3	21	1	ACL44999
C 19	16	20.8	20	1	AAQ48824
C 20	15.8	20.5	21	1	ADZ97584
C 21	15.4	20.0	21	1	ACL44498
C 22	15.4	20.0	22	1	ADD35279
C 23	15.2	19.7	20	1	ADK72854
C 24	15.2	19.7	20	1	ADK72874
C 25	14.8	19.2	20	1	ABL44489
C 26	14.8	19.2	21	1	AAQ35822
C 27	14.8	19.2	21	1	ADT92489
C 28	14.8	19.2	21	1	ADS93548
C 29	14.8	19.2	21	1	ACL44492
C 30	14.4	18.7	17	1	ABN10034
C 31	14.4	18.7	17	1	ABN10035
C 32	14.4	18.7	17	1	ACN73125
C 33	14.4	18.7	17	1	ACN73124

C 34	14.4	18.7	18	1	AAZ31818	Human G-alpha-13 a
C 35	14.2	18.4	20	1	ADK74660	Chimeric phosphoro
C 36	14.2	18.4	20	1	ADK73231	Chimeric phosphoro
C 37	14.2	18.4	20	1	ADP12043	Set 2 right PCR pr
C 38	14	18.2	17	1	ABN10033	Human GDMPL-1 17-m
C 39	14	18.2	17	1	ABN10032	Human GDMPL-1 17-m
C 40	14	18.2	17	1	ACN73122	Human GDMPL-1 prob
C 41	14	18.2	17	1	ACN73123	Human GDMPL-1 prob
C 42	13.8	17.9	17	1	ADC04443	Human Na/H exchang
C 43	13.4	17.4	15	1	ADJ82395	KLMSY-encoding nuc
C 44	13.4	17.4	17	1	ABN10036	Human GDMPL-1 17-m
C 45	13.4	17.4	17	1	ABT38020	Tumour suppression
C 46	13.4	17.4	17	1	ADC04444	Human Na/H exchang
C 47	13.4	17.4	17	1	ADC04445	Human Na/H exchang
C 48	13.4	17.4	17	1	ADB45419	Tumour suppression
C 49	13.4	17.4	17	1	ADI51144	Human tumour suppr
C 50	13.4	17.4	17	1	ACC53710	Human tumour suppr
C 51	13.4	17.4	17	1	ACN73126	Human GDMPL-1 prob
C 52	13.2	17.1	18	1	AAQ55741	LCR Oligo A. Synt
C 53	13.2	17.1	18	1	AAQ55744	LCR Oligo D. Synt
C 54	13.2	17.1	18	1	AAT14934	Oligo A probe for
C 55	13.2	17.1	18	1	AAT14937	Oligo D probe for
C 56	13.2	17.1	18	1	AAD13161	Human MTSPI protea
C 57	13.2	17.1	18	1	AAD36932	Human MTSPI protea
C 58	13.2	17.1	18	1	ADA25180	Human MTSPI sense
C 59	13.2	17.1	18	1	ADM57469	M. tuberculosis PC
C 60	13	16.9	15	1	ADJ82396	KLMSY-encoding nuc
C 61	13	16.9	17	1	ABN10031	Human GDMPL-1 17-m
C 62	13	16.9	17	1	ACN73121	Human GDMPL-1 prob
C 63	13	16.9	18	1	AAQ35522	PCR primer used to
C 64	12.8	16.6	17	1	ADC04442	Human Na/H exchang
C 65	12.8	16.6	17	1	ADB45336	Tumour suppression
C 66	12.8	16.6	18	1	AAC68677	Chick R35 RNA fing
C 67	12.8	16.6	18	1	ADG14616	Human CTLA-4 exon
C 68	12.8	16.6	18	1	ADL25789	Human cancer suppr
C 69	12.8	16.6	18	1	ADR474794	Allele specific pr
C 70	12.4	16.1	15	1	ADV37028	Human anti-HER2 NC
C 71	12.4	16.1	17	1	ADV64524	Human Her2 class I
C 72	12.4	16.1	17	1	ABN10037	Human GDMPL-1 17-m
C 73	12.4	16.1	17	1	ABZ65329	Human HER2 DNzyme
C 74	12.4	16.1	17	1	ADC04446	Human Na/H exchang
C 75	12.4	16.1	17	1	ADC04441	Human Na/H exchang
C 76	12.4	16.1	17	1	ADC04440	Human Na/H exchang
C 77	12.4	16.1	17	1	ADI47813	Human tumour suppr
C 78	12.4	16.1	17	1	ABE58478	Human VEGF recepto
C 79	12.4	16.1	17	1	ACN73127	Human GDMPL-1 prob
C 80	12.4	16.1	17	1	ADX59138	Human liver cancer
C 81	12.4	16.1	17	1	ADZ34403	Human HER2 substra
C 82	12.2	15.8	17	1	AAA23004	Integrin subunit b
C 83	12.2	15.8	17	1	ADV05926	Human BACE DNzyme
C 84	12.2	15.8	17	1	ADV05024	Human BACE zinzyme
C 85	12.2	15.8	17	1	ADV04194	Human BACE G-cleav
C 86	12.2	15.8	17	1	ADV06876	Human BACE ambery
C 87	12.2	15.8	17	1	ACN05922	WNV Amberzyme subs
C 88	12.2	15.8	17	1	ACN11559	NFKB sub-unit modu
C 89	12.2	15.8	17	1	ACA09006	NFKB minus strand I
C 90	12.2	15.8	17	1	ADA99321	Human MD23 scannin
C 91	12.2	15.8	17	1	ACC67819	Murine oligonucleo
C 92	12.2	15.8	17	1	ABE61480	Human VEGF recepto
C 93	12.2	15.8	17	1	ADM84037	DNA detection exte
C 94	12	15.6	12	1	ADM56305	Mouse SLC26A6 anio
C 95	12	15.6	16	1	ADR70044	Human survivin gen
C 96	12	15.6	16	1	ADM10034	Human survivin ant
C 97	12	15.6	16	1	ADM09555	Human survivin ant
C 98	12	15.6	16	1	ADM10035	Human survivin ant
C 99	12	15.6	16	1	ADM10037	Human survivin ant
C 100	12	15.6	16	1	ADM10036	Human survivin ant
C 101	12	15.6	17	1	ABN10030	Human GDMPL-1 17-m
C 102	12	15.6	17	1	ACN73120	Human GDMPL-1 prob
C 103	11.8	15.3	15	1	AAH18889	UCP3 polymorphism
C 104	11.8	15.3	15	1	AAFS2028	IGF-1 oligonucleot
C 105	11.8	15.3	15	1	ABL53810	Equine infectious
C 106	11.8	15.3	15	1	AAS19731	ASO probe #28 to d



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 16:10:20 ; Search time 0.001 Seconds  
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Perfect score: 77  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 100 seqs, 1463 residues

Total number of hits satisfying chosen parameters: 200

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : issdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	28.2	36.6	33	1	US-08-186-895-4
C 2	21	27.3	21	1	US-07-847-055A-13
C 3	21	27.3	21	1	US-08-403-888A-59
C 4	16	20.8	20	1	PCT-US96-09009-9
C 5	14.8	19.2	21	1	US-09-581-831-3
C 6	14.4	18.7	17	1	US-09-866-108A-10026
C 7	14.4	18.7	17	1	US-09-866-108A-10027
C 8	14.4	18.7	17	1	US-09-205-860-40
C 9	14	18.2	17	1	US-09-866-108A-10024
C 10	14	18.2	17	1	US-09-866-108A-10025
C 11	13.4	17.4	17	1	US-09-866-108A-10028
C 12	13.2	17.1	18	1	US-08-096-947-14
C 13	13.2	17.1	18	1	US-08-096-947-17
C 14	13.2	17.1	18	1	US-07-919-1408-14
C 15	13.2	17.1	18	1	US-07-919-1408-17
C 16	13.2	17.1	18	1	US-08-916-232-14
C 17	13.2	17.1	18	1	US-08-916-232-17
C 18	13.2	17.1	18	1	US-09-657-386B-6
C 19	13.2	17.1	18	1	PCT-US93-06939-14
C 20	13.2	17.1	18	1	PCT-US93-06939-17
C 21	13	16.9	17	1	US-09-866-108A-10023
C 22	12.4	16.1	17	1	US-09-474-432B-817
C 23	12.4	16.1	17	1	US-09-476-387-816
C 24	12.4	16.1	17	1	US-09-866-108A-10029
C 25	12	15.6	17	1	US-09-866-108A-10022
C 26	11.8	15.3	16	1	US-09-371-772B-6986
C 27	11.8	15.3	16	1	5168062-12
C 28	11.8	15.3	16	1	Patent No. 5168062
C 29	11.4	14.8	16	1	US-08-173-489C-4
C 30	11.2	14.5	16	1	US-08-308-892A-12
C 31	11.2	14.5	16	1	US-09-060-299-450
C 32	11.2	14.5	16	1	US-09-402-823A-450
C 33	11.2	14.5	16	1	US-09-798-542-9
C 34	11.2	14.5	16	1	Sequence 4, Appl
C 35	11.1	14.3	15	1	Sequence 13, Appl
C 36	10.8	14.0	15	1	Sequence 59, Appl
C 37	10.8	14.0	15	1	Sequence 9, Appl
C 38	10.8	14.0	15	1	Sequence 3, Appl
C 39	10.8	14.0	15	1	Sequence 10, Appl
C 40	10.8	14.0	15	1	Sequence 40, Appl
C 41	10.8	14.0	15	1	Sequence 10024, A
C 42	10.4	13.5	13	1	Sequence 10025, A
C 43	10	13.0	10	1	Sequence 10028, A
C 44	10	13.0	10	1	Sequence 14, Appl
C 45	10	13.0	10	1	Sequence 17, Appl
C 46	10	13.0	10	1	Sequence 14, Appl
C 47	10	13.0	10	1	Sequence 17, Appl
C 48	10	13.0	10	1	Sequence 14, Appl
C 49	10	13.0	10	1	Sequence 17, Appl
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C 61	10	13.0	10	1	Sequence 17, Appl
C 62	9.8	12.7	13	1	Sequence 14, Appl
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C 64	9.8	12.7	13	1	Sequence 14, Appl
C 65	9.8	12.7	13	1	Sequence 17, Appl
C 66	9.8	12.7	14	1	Sequence 14, Appl
C 67	9.8	12.7	14	1	Sequence 17, Appl
C 68	9.8	12.7	14	1	Sequence 14, Appl
C 69	9.8	12.7	14	1	Sequence 17, Appl
C 70	9.8	12.7	14	1	Sequence 14, Appl
C 71	9.8	12.7	14	1	Sequence 17, Appl
C 72	9.8	12.7	14	1	Sequence 14, Appl
C 73	9.8	12.7	14	1	Sequence 17, Appl
C 74	9.8	12.7	14	1	Sequence 14, Appl
C 75	9.8	12.7	14	1	Sequence 17, Appl
C 76	9.8	12.7	14	1	Sequence 14, Appl
C 77	9.8	12.7	14	1	Sequence 17, Appl
C 78	9.8	12.7	14	1	Sequence 14, Appl
C 79	9.8	12.7	14	1	Sequence 17, Appl
C 80	9.8	12.7	14	1	Sequence 14, Appl
C 81	9.8	12.7	14	1	Sequence 17, Appl
C 82	9.8	12.7	14	1	Sequence 14, Appl
C 83	9.8	12.7	14	1	Sequence 17, Appl
C 84	9.8	12.7	14	1	Sequence 14, Appl
C 85	9.8	12.7	14	1	Sequence 17, Appl
C 86	9.8	12.7	14	1	Sequence 14, Appl
C 87	9.8	12.7	14	1	Sequence 17, Appl
C 88	9.4	12.2	11	1	Sequence 14, Appl
C 89	9.4	12.2	12	1	Sequence 17, Appl
C 90	9.4	12.2	13	1	Sequence 14, Appl
C 91	9.4	12.2	13	1	Sequence 17, Appl
C 92	9.4	12.2	13	1	Sequence 14, Appl
C 93	9.4	12.2	13	1	Sequence 17, Appl
C 94	9.4	12.2	13	1	Sequence 14, Appl
C 95	9.4	12.2	13	1	Sequence 17, Appl
C 96	9.4	12.2	13	1	Sequence 14, Appl
C 97	9.4	12.2	13	1	Sequence 17, Appl
C 98	9.4	12.2	13	1	Sequence 14, Appl
C 99	9.4	12.2	13	1	Sequence 17, Appl
C 100	9.4	12.2	13	1	Sequence 14, Appl

## ALIGNMENTS

RESULT 1

US-08-186-895-4/c  
 ; Sequence 4, Application US/08186895  
 ; Patent No. 553885  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hollis, Melvyn  
 ; APPLICANT: Needham, Maurice R.C.  
 ; APPLICANT: Gooding, Clare  
 ; APPLICANT: Grosveld, Franklin G.  
 ; TITLE OF INVENTION: Expression Systems  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cushman, Darby & Cushman  
 ; STREET: 1615 L Street, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20036-5601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/186,895  
 ; FILING DATE: 27-JAN-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/046,383  
 ; FILING DATE: 09-APR-1993  
 ; APPLICATION NUMBER: US/07/810,414  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kokulis, Paul N.  
 ; REGISTRATION NUMBER: 16,773  
 ; REFERENCE/DOCKET NUMBER: FWK/3893/93802/MJW  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-861-3000  
 ; TELEFAX: 202-822-0944  
 ; TELEX: 6714627 CUSH  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 33 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-186-895-4

Query Match 36.6%; Score 28.2; DB 1; Length 33;  
 Best Local Similarity 90.9%; Pred. No. 0.082;  
 Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 8 GAGGGCTGGGGATACAACTCTGGAGTCTCTG 40  
 Db 33 GACGGCTGGGGATACAACTCTGGAGTCTCTG 1

RESULT 2  
 US-08-186-895-4/c  
 ; Sequence 13, Application US/07847055A  
 ; Patent No. 5530114  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ISIS Pharmaceuticals  
 ; TITLE OF INVENTION: Oligonucleotide Modulation of  
 ; TITLE OF INVENTION: Arachidonic Acid Metabolism  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn  
 ; ADDRESSEE: Kurtz Mackiewicz & No. 5530114ris  
 ; STREET: One Liberty Place - 46th Floor  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19103

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: WORDPERFECT 5.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/847,055A  
 ; FILING DATE: 19920403  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/516,969  
 ; FILING DATE: April 30, 1990  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: John W. Caldwell  
 ; REGISTRATION NUMBER: 28,937  
 ; REFERENCE/DOCKET NUMBER: ISIS-182  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-3100  
 ; TELEFAX: (215) 568-3439  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 21  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; ANTI-SENSE: yes  
 ; US-07-847-055A-13

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 Best Local Similarity 100.0%; Pred. No. 0.94;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 20 ATCAACTCTGGAGTCTCTG 40  
 Db 21 ATCAACTCTGGAGTCTCTG 1

RESULT 3  
 US-08-403-888A-59/c  
 ; Sequence 59, Application US/08403888A  
 ; Patent No. 5952490  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hanecek et al.  
 ; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core  
 ; TITLE OF INVENTION: Sequence  
 ; NUMBER OF SEQUENCES: 146  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP  
 ; STREET: One Liberty Place - 46th Floor  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
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 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WordPerfect 6.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/403,888A  
 ; FILING DATE: 12-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/954,185  
 ; FILING DATE: 29-SEP-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Paul K. Legaard  
 ; REGISTRATION NUMBER: 38,534  
 ; REFERENCE/DOCKET NUMBER: ISIS-1229  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-568-3100  
 ; TELEFAX: 215-568-3439  
 ; INFORMATION FOR SEQ ID NO: 59:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-403-888A-59
Query Match 27.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATACAACCTCTGGATGCTCTG 40
Db 21 ATACAACCTCTGGATGCTCTG 1

RESULT 4
PCT-US96-09009-9/c
; GENERAL INFORMATION:
; APPLICANT: Buchberg, Arthur M.
; APPLICANT: Siracusa, Linda D.
; APPLICANT: Chepenik, Kenneth P.
; TITLE OF INVENTION: RISK FACTOR FOR COLORECTAL CANCER
; TITLE OF INVENTION: AND
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09009
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,359
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US96-09009-9
Query Match 20.8%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 CTGATGTCCTGTCAAG 77
Db 20 CTGATGTCCTGTCAAG 5

RESULT 5
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US-09-581-831-3
; Sequence 3, Application US/09581831
; Patent No. 6448020
; GENERAL INFORMATION:
; APPLICANT: TOFTGARD, RUNE
; APPLICANT: ZAPHIROPOULOS, PETER G.
; APPLICANT: KOGERMAN, PRIIT
; APPLICANT: GRIMM, THOMAS
; TITLE OF INVENTION: MOLECULES ASSOCIATED WITH THE HUMAN SUPPRESSOR OF FUSED
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 50695-60568
; CURRENT APPLICATION NUMBER: US/09/581,831
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: PCT/SE98/02383
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 9704788-0
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 9802293-2
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-581-831-3
Query Match 19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGCTCTGTCA 75
Db 1 GAAGCTGATGCTGTGCCA 18

RESULT 6
US-09-866-108A-10026
; Sequence 10026, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10026
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10026

Query Match      18.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAG 42
    |||||
Db 2 TCTGGAGTCTCTGTG 17

RESULT 7
US-09-866-108A-10027
; Sequence 10027, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10027
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10027

Query Match      18.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAG 42
    |||||
Db 1 TCTGGAGTCTCTGTG 16

; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10026
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10026

Query Match      18.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAG 42
    |||||
Db 1 TCTGGAGTCTCTGTG 16
```

```
RESULT 8
US-09-205-860-40/c
; Sequence 40, Application US/09205860
; Patent No. 5981732
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowseit
; TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
; FILE REFERENCE: RTS-0031
; CURRENT APPLICATION NUMBER: US/09/205,860
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-860-40
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```
Query Match      18.7%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 13 CCTGGGGATACAACTC 28
    |||||
Db 17 CCTGGGGAGACAACTC 2
```

```
RESULT 9
US-09-866-108A-10024
; Sequence 10024, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10024
; LENGTH: 17
; TYPE: DNA
```

```

; ORGANISM: Homo sapiens
US-09-866-108A-10024

Query Match      18.2%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCCTCTG 40
    |||||
Db 4 TCTGGAGTCCTCTG 17

RESULT 10
US-09-866-108A-10025
; Sequence 10025, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10025
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10028

Query Match      17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGGAGTCCTCTGAG 42
    |||||
Db 1 CTGGAGTCCTCTG 15

RESULT 12
US-08-096-947-14/c
; Sequence 14, Application US/08096947
; Patent No. 5506137
; GENERAL INFORMATION:
; APPLICANT: Eric J. Mathur
; APPLICANT: Edward J. Marsh
; APPLICANT: Warren E. Schoettlin
; TITLE OF INVENTION: Purified Thermostable
; TITLE OF INVENTION: Pyrococcus Furiosus DNA
; TITLE OF INVENTION: Ligase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0

```

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,947
; FILING DATE: 19930722
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/919,140
; FILING DATE: July 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: STRG 20081 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: 278356
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-08-096-947-14

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACAACCTTGGAGTC 1

RESULT 13
US-08-096-947-17
; Sequence 17, Application US/08096947
; Patent No. 5506137
; GENERAL INFORMATION:
; APPLICANT: Eric J. Mathur
; APPLICANT: Edward J. Marsh
; APPLICANT: Warren E. Schoettlin
; TITLE OF INVENTION: Purified Thermostable
; TITLE OF INVENTION: Pyrococcus DNA
; TITLE OF INVENTION: Ligase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,947
; FILING DATE: 19930722
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/919,140
; FILING DATE: July 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: STRG 20081 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
;

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACAACCTTGGAGTC 1
```

```
;
; TELEX: 278356
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-08-096-947-17

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 1 GGACACAACCTTGGAGTC 18

RESULT 14
US-07-919-140B-14/c
; Sequence 14, Application US/07919140B
; Patent No. 5700672
; GENERAL INFORMATION:
; APPLICANT: Eric J. Mathur
; APPLICANT: Edward J. Marsh
; APPLICANT: Warren E. Schoettlin
; TITLE OF INVENTION: Purified Thermostable Pyrococcus
; TITLE OF INVENTION: Furiosus DNA Ligase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/919,140B
; FILING DATE: July 23, 1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-07-919-140B-14

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 18 GGATACAACTCTGGAGTC 35
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Db 18 GGACACAACTTGGAGTC 1

## RESULT 15

US-07-919-140B-17  
; Sequence 17, Application US/07919140B  
; Patent No. 5700872  
; GENERAL INFORMATION:  
; APPLICANT: Eric J. Mathur  
; APPLICANT: Edward J. Marsh  
; APPLICANT: Warren E. Schoettlin  
; TITLE OF INVENTION: Purified Thermostable Pyrococcus  
; TITLE OF INVENTION: Purified Thermostable Pyrococcus  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 2730 Sand Hill Road  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/919,140B  
; FILING DATE: July 23, 1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Albert P. Halluin  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8142-013  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
US-07-919-140B-17

Query Match 17.1%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 18;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGTC 35  
||| ||||| ||||| |||||  
Db 1 GGACACAACTTGGAGTC 18

## RESULT 16

US-08-916-232-14/c  
; Sequence 14, Application US/08916232  
; Patent No. 6280998  
; GENERAL INFORMATION:  
; APPLICANT: Eric J. Mathur  
; APPLICANT: Edward J. Marsh  
; APPLICANT: Warren E. Schoettlin  
; TITLE OF INVENTION: Purified Thermostable Pyrococcus  
; TITLE OF INVENTION: Purified Thermostable Pyrococcus  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 2730 Sand Hill Road  
; CITY: Menlo Park

; STATE: California  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,232  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/919,140  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Albert P. Halluin  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8142-013  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
US-08-916-232-14

Query Match 17.1%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 18;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGTC 35  
||| ||||| ||||| |||||  
Db 18 GGACACAACTTGGAGTC 1

## RESULT 17

US-08-916-232-17  
; Sequence 17, Application US/08916232  
; Patent No. 6280998  
; GENERAL INFORMATION:  
; APPLICANT: Eric J. Mathur  
; APPLICANT: Edward J. Marsh  
; APPLICANT: Warren E. Schoettlin  
; TITLE OF INVENTION: Purified Thermostable Pyrococcus  
; TITLE OF INVENTION: Purified Thermostable Pyrococcus  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 2730 Sand Hill Road  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,232  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/919,140  
; FILING DATE:

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-08-916-232-17

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 1 GGACACAACTTGGAGTC 18

RESULT 18
US-09-657-986B-6/c
; Sequence 6, Application US/09657986B
; Patent No. 6797504
; GENERAL INFORMATION:
; APPLICANT: Madison, Edwin L.
; APPLICANT: Semple, Joseph Edward
; APPLICANT: Coombs, Gary Samuel
; APPLICANT: Reiner, John Eugene
; APPLICANT: Ong, Edgar O.
; APPLICANT: Araldi, Gian Luca
; TITLE OF INVENTION: Inhibitors of Serine Protease Activity of Matriptase or
; FILE REFERENCES: Corvas 255/049
; CURRENT APPLICATION NUMBER: US/09/657,986B
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: oligonucleotide primer
; US-09-657-986B-6

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 30 GGAGTCCTCTGAGAGGTA 47
Db 18 GGAGTCCTGAGAGGTA 1

RESULT 19
PCT-US93-06939-14/c
; Sequence 14, Application PC/TUS9306939
; GENERAL INFORMATION:
; APPLICANT: Eric J. Mathur
; APPLICANT: Edward J. Marsh
; APPLICANT: Warren E. Schoettlin
; TITLE OF INVENTION: Purified Thermostable
; TITLE OF INVENTION: Pyrococcus Furiosus DNA
```

```
; TITLE OF INVENTION: Ligase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06939
; FILING DATE: 19930722
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/919,140
; FILING DATE: July 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: STRG 20081 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: 278356
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; PCT-US93-06939-14

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACAACTTGGAGTC 1

RESULT 20
PCT-US93-06939-17
; Sequence 17, Application PC/TUS9306939
; GENERAL INFORMATION:
; APPLICANT: Eric J. Mathur
; APPLICANT: Edward J. Marsh
; APPLICANT: Warren E. Schoettlin
; TITLE OF INVENTION: Purified Thermostable
; TITLE OF INVENTION: Pyrococcus Furiosus DNA
; TITLE OF INVENTION: Ligase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
```



```
; APPLICATION NUMBER: PCT/US93/06939
; FILING DATE: 19930722
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/919,140
; FILING DATE: JULY 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: STRG 20081 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: 278356
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; PCT-US93-06939-17

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
DB 1 GGACACAACTTGGAGTC 18

RESULT 21
US-09-866-108A-10023
; Sequence 10023, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15/55
; SOFTWARE: Acomica Sequence Listing Engine
```

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; Patent No. 6686188
; SEQ ID NO 10023
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10023

Query Match 16.9%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCT 39
DB 5 TCTGGAGTCTCTCT 17

RESULT 22
US-09-474-432B-817
; Sequence 817, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MEHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 817
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-817

Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 28 CTGGAGTCTCTCTCA 41
DB 4 CUGGAGCCUCUGA 17

RESULT 23
US-09-476-387-816
; Sequence 816, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their incorporation into Oligonucleoti
; FILE REFERENCE: MEHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
```

```
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 816
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-476-387-816

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      28 CTGGAGTCTCTG 41
Db      4 CUGGAGCCUCUGA 17

RESULT 24
US-09-866-108A-10029
; Sequence 10029, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: GB 24263.6
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10029
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-10029

Query Match      15.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 TCTGGAGTCTCTC 38
Db      6 TCTGGAGTCTCTC 17

RESULT 26
US-09-371-772B-6986/c
; Sequence 6986, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
```

```
Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      29 TGGAGTCTCTGAG 42
Db      1 TGGAGTCTCTGTG 14

RESULT 25
US-09-866-108A-10022
; Sequence 10022, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10022
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-10022

Query Match      15.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 TCTGGAGTCTCTC 38
Db      6 TCTGGAGTCTCTC 17

RESULT 26
US-09-371-772B-6986/c
; Sequence 6986, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
```

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6986
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6986

Query Match      15.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 28;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      52 GCCAGCGAGCTGAT 66
Db      16 GCCAGCATGCTGAT 2

RESULT 27
5168062-12/c
; Patent No. 5168062
; APPLICANT: STINSKI, MARK F.
; TITLE OF INVENTION: TRANSFER VECTORS AND MICROORGANISMS
; CONTAINING HUMAN CYTOMEGALOVIRUS IMMEDIATE-EARLY
; PROMOTER-REGULATORY DNA SEQUENCE
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/582,130
; FILING DATE: 10-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 256,134
; FILING DATE: 5-OCT-1988
; APPLICATION NUMBER: 58,662
; FILING DATE: 22-MAY-1987
; APPLICATION NUMBER: 696,617
; FILING DATE: 30-JAN-1985
; SEQ ID NO:12:
; LENGTH: 16
5168062-12

Query Match      15.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 28;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      63 TGATGTCCTGTCAG 77
Db      15 TGATGTAAGTCCCAAG 1

RESULT 28
5168062-13/c
; Patent No. 5168062
; APPLICANT: STINSKI, MARK F.
; TITLE OF INVENTION: TRANSFER VECTORS AND MICROORGANISMS
; CONTAINING HUMAN CYTOMEGALOVIRUS IMMEDIATE-EARLY
; PROMOTER-REGULATORY DNA SEQUENCE
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/582,130
; FILING DATE: 10-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 256,134
; FILING DATE: 5-OCT-1988
```

```
; APPLICATION NUMBER: 58,662
; FILING DATE: 22-MAY-1987
; APPLICATION NUMBER: 696,617
; FILING DATE: 30-JAN-1985
; SEQ ID NO:13:
; LENGTH: 16
5168062-13

Query Match      15.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 28;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      63 TGATGTCCTGTCAG 77
Db      15 TGATGTAAGTCCCAAG 1

RESULT 29
US-08-173-489C-4/c
; Sequence 4, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: Nucleic Acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from c-myc
; DESCRIPTION: sequence region in Seq ID No. 58612443
; HYPOTHETICAL: Yes
; ANTI-SENSE: No
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 4 :FROM 1 TO 16
US-08-173-489C-4

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      40 GAGAGGTAAGAG 52
```

```
Db      14 GACAGGGAAGAG 2
||||| |||||
STATE: Virginia
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,299
FILING DATE: 15-APR-1998
CLASSIFICATION: 435
TITLE OF INVENTION: SPECIES-SPECIFIC DETECTION OF MYCOBACTERIUM KANSASII
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and Company
ADDRESS: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/308,892A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3128
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-308-892A-12

Query Match      14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 AACAAAGACGGCCTGGG 18
||||| ||||| ||
Db      1 AACTCGAGCGGCTCGG 16

RESULT 31
US-09-060-299-450
; Sequence 450, Application US/09060299
; Patent No. 6545137
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; Hesse, John W
; Caskey, Charles T
; Cox, Roger D
; Gerhold, David
; Hammond, Holly
; Hey, Patricia
; Kawaguchi, Yoshihiko
; Merriman, Tony R
; Metzker, Michael L
; TITLE OF INVENTION: No. 6545137el Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001

Db      1 TCACAGGTAAGGAGCC 16
||||| ||||| |||||
QY      39 TCACAGGTAAGGAGCC 54
||||| ||||| |||||
Db      1 TCACAGGTAAGGAGCC 16

RESULT 32
US-09-402-923A-450
; Sequence 450, Application US/09402923A
; Patent No. 6555654
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; Hesse, John W
; Caskey, Charles T
; Cox, Roger D
; Gerhold, David
; Hammond, Holly
; Hey, Patricia
; Kawaguchi, Yoshihiko
; Merriman, Tony R
; Metzker, Michael L
; TITLE OF INVENTION: No. 6555654el LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 450:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 450:
US-09-402-923A-450

Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAGAGCC 54
Db 1 TCACAGGTAAGAGCC 16

RESULT 33
US-09-798-542-9/c
; Sequence 9, Application US/09798542
; Patent No. 6685948
; GENERAL INFORMATION:
; APPLICANT: Zeng, Lingling
; TITLE OF INVENTION: REPLICATION-DEFECTIVE DENGUE VIRUSES
; TITLE OF INVENTION: THAT ARE REPLICATION-DEFECTIVE IN MOSQUITOES FOR USE AS
; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: NIH145.001C1
; CURRENT APPLICATION NUMBER: US/09/798,542
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/US 99/02598
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 60/098,981
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Flavivirus, West Nile
US-09-798-542-9

Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 26 CTCGGAGTCTCTGA 41
Db 16 CTCGTGTCTCTATGA 1

RESULT 34
US-09-875-453B-65/c
; Sequence 65, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELEPHONE: (213) 489-1600

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```

; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongsachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135 US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453B-65

Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 38 CTGAGAGGTAAGAGC 53
Db 16 CTCGGAGGTGGAGGC 1

RESULT 35
US-08-363-240A-116/c
; Sequence 116, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwigen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELEPHONE: (213) 489-1600

```

TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 116:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-363-240A-116

Query Match 14.3%; Score 11; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 GTCCTCTGAGA 43  
 Db 15 GTCCTCTGAGA 5

## RESULT 36

US-08-182-968A-186/c  
 Sequence 186, Application US/08182968A

Patent No. 5610054  
 GENERAL INFORMATION:  
 APPLICANT: Draper, Kenneth G.  
 TITLE OF INVENTION: METHOD AND REAGENT FOR  
 TITLE OF INVENTION: INHIBITING HEPATITIS C  
 TITLE OF INVENTION: VIRUS REPLICATION  
 NUMBER OF SEQUENCES: 497  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/182,968A  
 FILING DATE: 13-JANUARY-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/882,888  
 FILING DATE: 14-MAY-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 205/277  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 186:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-182-968A-186

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 38;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGTC 70  
 Db 15 CCAAGATGATGTC 2

## RESULT 37

US-08-319-492B-357/c  
 Sequence 357, Application US/08319492B

Patent No. 5616488  
 GENERAL INFORMATION:  
 APPLICANT: Sullivan, Sean M.  
 APPLICANT: Draper, Kenneth G.  
 APPLICANT: McSwiggen, James  
 APPLICANT: Stinchcomb, Dan T.  
 TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
 TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS  
 TITLE OF INVENTION: OF IL-5  
 NUMBER OF SEQUENCES: 751  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/319,492B  
 FILING DATE: October 7, 1994

PRIOR APPLICATION DATA:  
 PRIOR APPLICATION DATA: including application  
 PRIOR APPLICATION DATA: described below:  
 APPLICATION NUMBER: 08/008,895  
 FILING DATE: January 19, 1993  
 APPLICATION NUMBER: 07/989,849  
 FILING DATE: December 7, 1992  
 ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 209/276  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 357:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-319-492B-357

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 38;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 25 ACTCTGAGTCTTC 38  
 Db 14 ACTCTGAGTCTTC 1

## RESULT 38

US-08-319-492B-358/c  
 Sequence 358, Application US/08319492B

Patent No. 5616488  
 GENERAL INFORMATION:  
 APPLICANT: Sullivan, Sean M.  
 APPLICANT: Draper, Kenneth G.  
 APPLICANT: McSwiggen, James  
 APPLICANT: Stinchcomb, Dan T.  
 TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES

## ; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS

; NUMBER OF SEQUENCES: OF IL-5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/319,492B

; FILING DATE: October 7, 1994

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/276

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 358:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-319-492B-358

Two

Query Match 14.0%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 38;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 ACTCTGAGTCCTC 38

Db 14 ACTCTGAAGTCCTC 1

## RESULT 39

US-08-291-932A-373

; Sequence 373, Application US/08291932A

; Patent No. 5658780

; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Dan T.

; APPLICANT: Draper, Kenneth G.

; APPLICANT: McSwiggen, James

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: NF-KB

; NUMBER OF SEQUENCES: 830

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/291,932A

; FILING DATE: August 15, 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/245,466

; FILING DATE: May 18, 1994

; APPLICATION NUMBER: 07/987,132

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/157

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 373:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-291-932A-373

Query Match 14.0%; Score 10.8; DB 1; Length 15;

Best Local Similarity 64.3%; Pred. No. 38;

Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTGAG 42

Db 2 UGGAGUACCCUGAG 15

## RESULT 40

US-08-774-306A-186/c

; Sequence 186, Application US/08774306A

; Patent No. 5869253

; GENERAL INFORMATION:

; APPLICANT: Draper, Kenneth G.

; TITLE OF INVENTION: METHOD AND REAGENT FOR

; TITLE OF INVENTION: INHIBITING HEPATITIS C

; TITLE OF INVENTION: VIRUS REPLICATION

; NUMBER OF SEQUENCES: 497

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/774,306A

; FILING DATE: December 26, 1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/182,968

; FILING DATE: January 13, 1994

; APPLICATION NUMBER: 07/882,888

Two





```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA: US/08/171.385
APPLICATION NUMBER: US/08/171.385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-171-385-28

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 44
US-08-351-748-13
Sequence 13 Application US/08351748
Patent No. 5599672
GENERAL INFORMATION:
APPLICANT: Liang, Peng
APPLICANT: Pardee, Arthur B.
APPLICANT: Bianchi, Cesario P.
TITLE OF INVENTION: IDENTIFYING, ISOLATING, AND CLONING
TITLE OF INVENTION: MESSENGER RNAS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHOATE, HALL & STEWART
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,748
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,084

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA: US/08/171.385
APPLICATION NUMBER: US/08/171.385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-171-385-28

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 45
US-08-430-536A-13
Sequence 13 Application US/08430536A
Patent No. 566547
GENERAL INFORMATION:
APPLICANT: Liang, Peng
APPLICANT: Pardee, Arthur B.
TITLE OF INVENTION: IDENTIFYING, ISOLATING, AND CLONING
TITLE OF INVENTION: MESSENGER RNAS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHOATE, HALL & STEWART
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,536A
FILING DATE: 25-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Herschbach Ph.D., Brenda M.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 181411-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
TELEFAX: (617) 248-4000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-430-536A-13

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 45
US-08-430-536A-13
Sequence 13 Application US/08430536A
Patent No. 566547
GENERAL INFORMATION:
APPLICANT: Liang, Peng
APPLICANT: Pardee, Arthur B.
TITLE OF INVENTION: IDENTIFYING, ISOLATING, AND CLONING
TITLE OF INVENTION: MESSENGER RNAS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHOATE, HALL & STEWART
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,536A
FILING DATE: 25-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Herschbach Ph.D., Brenda M.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 181411-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
TELEFAX: (617) 248-4000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-430-536A-13

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 46
US-08-463-660-14
; Sequence 14, Application US/08463660
; Patent No. 5759776
; GENERAL INFORMATION:
; APPLICANT: SMITH, HELENE S.
; APPLICANT: CHEN, LING-CHUN
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND TREATMENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,660
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 28888-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-463-660-14

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 47
US-08-678-280-14
; Sequence 14, Application US/08678280
; Patent No. 5776683
; GENERAL INFORMATION:
; APPLICANT: SMITH, HELENE S.
; APPLICANT: CHUN, LING-CHEN
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND
; TREATMENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018

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```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,280
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 28888-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-678-280-14

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 48
US-08-582-261A-4
; Sequence 4, Application US/08582261A
; Patent No. 5817461
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard C.
; APPLICANT: Hirsh, Jack
; APPLICANT: Weitz, Jeff
; TITLE OF INVENTION: Methods and Compositions for Diagnosis
; TITLE OF INVENTION: of Hyperhomocysteinemia
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,261A
; FILING DATE: 03-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 016558-001200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

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; TOPOLOGY: linear
; US-08-582-261A-4
;
; Query Match 13.0%; Score 10; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 35;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 49
US-08-684-547-13
; Sequence 13, Application US/08684547
; Patent No. 5965409
; GENERAL INFORMATION:
; APPLICANT: Pardee Ph.D., Arthur B.
; TITLE OF INVENTION: SYSTEM FOR COMPARING LEVELS OR AMOUNTS
; OF INVENTION: OF mRNAs
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,547
; FILING DATE: 19-JUL-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0181411-0013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248-4000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-684-547-13

; Query Match 13.0%; Score 10; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 35;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 50
US-08-942-819-3
; Sequence 3, Application US/08942819
; Patent No. 5965707
; GENERAL INFORMATION:
; APPLICANT: Tam, See-Ying
; APPLICANT: Tsai, Mindy
; APPLICANT: Galli, Stephen J.
; TITLE OF INVENTION: RIN2, A NOVEL INHIBITOR OF

```

```

; TITLE OF INVENTION: RAS-MEDIATED SIGNALING
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/942,819
; FILING DATE: 02-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/058,520
; FILING DATE: 11-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BIH96-13pa
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-942-819-3

; Query Match 13.0%; Score 10; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 35;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 51
US-08-361-441B-28
; Sequence 28, Application US/08361441B
; Patent No. 6077948
; GENERAL INFORMATION:
; APPLICANT: Russell, Mary E.
; APPLICANT: Utans, Ulrike
; TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,441B
; FILING DATE: 21-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/171,385

```



;; GENERAL INFORMATION:  
;; APPLICANT: Tam, See-Ying  
;; APPLICANT: Tsai, Mindy  
;; APPLICANT: Galli, Stephen J.  
;; TITLE OF INVENTION: RIN2, A NOVEL INHIBITOR OF RAS-MEDICATED  
;; TITLE OF INVENTION: SIGNALING  
;; FILE REFERENCE: 1440.1089-004  
;; CURRENT APPLICATION NUMBER: US/09/522,955A  
;; CURRENT FILING DATE: 2000-03-10  
;; PRIOR APPLICATION NUMBER: PCT/US98/19056  
;; PRIOR FILING DATE: 1998-09-11  
;; PRIOR APPLICATION NUMBER: US 08/942,819  
;; PRIOR FILING DATE: 1997-10-02  
;; PRIOR APPLICATION NUMBER: US 60/058,520  
;; PRIOR FILING DATE: 1997-09-11  
;; NUMBER OF SEQ ID NOS: 23  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 10  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-522-955A-3

Query Match 13.0%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60  
|||||  
Db 1 AGCCAGCGAA 10

RESULT 56  
PCT-US93-02246-13  
; Sequence 13, Application PC/TUS9302246  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Peng  
; APPLICANT: Pardee, Arthur B.  
; TITLE OF INVENTION: Identifying, Isolating and Cloning  
; TITLE OF INVENTION: Messenger RNAs  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Choate, Hall & Stewart  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02190  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/02246  
; FILING DATE: 19930311  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/850,343  
; FILING DATE: 11-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pasternack, Sam  
; REGISTRATION NUMBER: 29,576  
; REFERENCE/DOCKET NUMBER: DFC1234CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617 227-5020  
; TELEFAX: 617 227-7566  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: NUCLEIC ACID

;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: other nucleic acid  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
PCT-US93-02246-13

Query Match 13.0%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60  
|||||  
Db 1 AGCCAGCGAA 10

RESULT 57  
US-09-674-913B-14  
; Sequence 14, Application US/09674913B  
; Patent No. 6861057  
; GENERAL INFORMATION:  
; APPLICANT: Gaudernack, Gustav  
; APPLICANT: Eriksen, Jon Amund  
; APPLICANT: Moller, Mona  
; TITLE OF INVENTION: Frameshift Mutants of Beta-Amyloid Precursor Protein and Ubiquitin  
; TITLE OF INVENTION: Their Use  
; FILE REFERENCE: 001702.401600  
; CURRENT APPLICATION NUMBER: US/09/674,913B  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: PCT/NO99/00141  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: NO 19982098  
; PRIOR FILING DATE: 1998-05-08  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-674-913B-14

Query Match 13.0%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TCTGAGAGGT 46  
|||||  
Db 1 TCTGAGAGGT 10

RESULT 58  
US-08-221-968-2/c  
; Sequence 2, Application US/08221968  
; Patent No. 5472843  
; GENERAL INFORMATION:  
; APPLICANT: Millman, Curt L.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES TO HAEMOPHILUS INFLUENZAE  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,968  
; FILING DATE:

```
/ CLASSIFICATION: 435
/ PRIOR APPLICATION NUMBER: US 07/690,788
/ FILING DATE: 25-APR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 193/119
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 213-489-1600
/ TELEFAX: 213-955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-08-221-968-2

Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AGCGAGCTG 64
Db 12 AGCGAGCTG 3

RESULT 59
US-08-567-196-2/c
; Sequence 2, Application US/08567196
; Patent No. 5830654
; GENERAL INFORMATION:
; APPLICANT: Milliman, Curt L.
; TITLE OF INVENTION: NUCLEIC ACID PROBES TO HAEMOPHILUS
; TITLE OF INVENTION: INFLUENZA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,196
; FILING DATE: 04-DEC-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/690,788
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 193/119
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
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US-08-567-196-2

Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AGCGAGCTG 64
Db 12 AGCGAGCTG 3

RESULT 60
US-08-985-162-1837/c
; Sequence 1837, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1837:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-985-162-1837

Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGAGCCAGCG 58
Db 14 AGAGCCAGCG 5

RESULT 61
US-09-401-063-1837/c
; Sequence 1837, Application US/09401063
```

Patent No. 6623962  
 GENERAL INFORMATION:  
 APPLICANT: Akhtar, Saghir  
 APPLICANT: Fell, Patricia  
 APPLICANT: McSwiggen, James  
 TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT  
 TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED  
 TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH  
 TITLE OF INVENTION: FACTOR RECEPTORS  
 NUMBER OF SEQUENCES: 1877  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/401,063  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/985,162  
 FILING DATE: 04 December 1997  
 APPLICATION NUMBER: 60/036,476  
 FILING DATE: 31 January 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 230/107  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 1837:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-401-063-1837

Query Match 13.0%; Score 10; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGAGCCGCG 58  
 |||||  
 Db 14 AGAGCCGCG 5

RESULT 62  
 US-08-615-961-8  
 Sequence 8, Application US/08615961  
 Patent No. 5877162  
 GENERAL INFORMATION:  
 APPLICANT: Martina Werner and Shaji T. George  
 TITLE OF INVENTION: Short External Guide Sequences  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 2800 One Atlantic Center  
 STREET: 1201 West Peachtree Street  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA

ZIP: 30309-3450  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/615,961  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: IL1115  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404) 873-8794  
 TELEFAX: (404) 873-8795  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: RNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-615-961-8

Query Match 12.7%; Score 9.8; DB 1; Length 13;  
 Best Local Similarity 69.2%; Pred. No. 48;  
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGCCTGGGGATAC 23  
 |||:|||||  
 Db 1 GGUUGGGGAUAC 13

RESULT 63  
 US-08-867-820A-49/c  
 Sequence 49, Application US/0867820A  
 Patent No. 5891685  
 GENERAL INFORMATION:  
 APPLICANT: YAMAGISHI Masahiro  
 APPLICANT: TAKAI Yukie  
 APPLICANT: MIKAWA Takashi  
 APPLICANT: HARA Mari  
 APPLICANT: UEDA Makoto  
 APPLICANT: OHARA Akiko  
 TITLE OF INVENTION: METHOD FOR PRODUCING ESTER OF (S) - -HALOGENATED- -HYDROXYBUTY  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.  
 STREET: 2033 K Street, N.W., Suite 800  
 CITY: Washington, D.C.  
 COUNTRY: USA  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/867,820A  
 FILING DATE: June 3, 1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee Cheng  
 REGISTRATION NUMBER: 40,949  
 REFERENCE/DOCKET NUMBER: 1416/OP574US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-721-8200  
 TELEFAX: 202-721-8250  
 INFORMATION FOR SEQ ID NO: 49:

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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ ORIGINAL SOURCE:
/ ORGANISM: Selenophoma donacis
/ STRAIN: CBS417.51
US-08-867-820A-49

Query Match 12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 60 AGCTGATGTCCTG 72
Db 13 AGCTGATGACTTG 1

RESULT 64
US-08-729-601A-7/c
/ Sequence 7, Application US/08729601A
/ Patent No. 6166302
/ GENERAL INFORMATION:
/ APPLICANT: Merlo, Donald J.
/ TITLE OF INVENTION: Modified Bacillus Thuringiensis Gene for
/ TITLE OF INVENTION: Lepidopteran Control in Plants
/ NUMBER OF SEQUENCES: 84
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fitch, Even, Tabin & Flannery
/ STREET: 135 S. LaSalle St.
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/729,601A
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Krueger, James P.
/ REGISTRATION NUMBER: 35,234
/ REFERENCE/DOCKET NUMBER: 60089
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-372-7842
/ TELEFAX: 312-372-7848
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
US-08-729-601A-7

Query Match 12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 CTCTGGAGTCCTC 38
Db 13 CTCTAGAGTCCCC 1

RESULT 65
US-08-679-645-1247/c
/ Sequence 1247, Application US/08679645
/ Patent No. 6350934
/ GENERAL INFORMATION:
/ APPLICANT: Zwick, Michael G.
/ APPLICANT: Edington, Brent E.
/ APPLICANT: McSwiggen, James A.
/ APPLICANT: Merlo, Patricia Ann Owens
/ APPLICANT: Guo, Lining
/ APPLICANT: Skokut, Thomas A.
/ APPLICANT: Young, Scott A.
/ APPLICANT: Folkerts, Otto
/ APPLICANT: Merlo, Donald J.
/ TITLE OF INVENTION: COMPOSITION AND METHODS FOR
/ TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
/ TITLE OF INVENTION: IN PLANTS
/ NUMBER OF SEQUENCES: 1263
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/679,645
/ FILING DATE: July 12, 1996
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/001,135
/ FILING DATE: July 13, 1995
/ APPLICATION NUMBER: 08/300,726
/ FILING DATE: September 2, 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 219/247
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 1247:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-679-645-1247

Query Match 12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 CTCTGGAGTCCTC 38
Db 13 CTCTAGAGTCCCC 1

RESULT 66
US-08-233-608-26/c
/ Sequence 26, Application US/08233608
/ Patent No. 5585238
/ GENERAL INFORMATION:
/ APPLICANT: Ligon, James M
/ APPLICANT: Beck, James J
/ TITLE OF INVENTION: Detection of Fungal Pathogens Using the
/ TITLE OF INVENTION: Polymerase Chain Reaction
```



NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ciba-Geigy Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/233,608  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: CGC 1739  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8615  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: Oligonucleotide primer JB443  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-233-608-26

Query Match 12.7%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 51;  
Matches 11; Conservative 0; Mismatches 2; Indels

Qy 7 AGACGGCCTGGGG 19  
Db 13 AGACGGCCTCCGG 1

RESULT 67  
US-08-271-880A-49/c  
; Sequence 49, Application US/08271880A  
; Patent No. 5693535  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth G. Draper  
; APPLICANT: Bharat Chowrira  
; APPLICANT: James McSwiggen  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James D. Thompson  
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS  
; TITLE OF INVENTION: REPLICATION  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/271,880A  
 FILING DATE: July 7, 1994  
 PRIOR APPLICATION DATA:  
 PRIOR APPLICATION DATA: including application  
 PRIOR APPLICATION DATA: described below:  
 APPLICATION NUMBER: 08/103,443  
 FILING DATE: August 6, 1993  
 APPLICATION NUMBER: 07/882,886  
 FILING DATE: May 14, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warzburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 206/116  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 49:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-271-880A-49

Query Match 12.7%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 51;  
Matches 11; Conservative 0; Mismatches 2; Indels

QY . 59 AAGCTGATGTCTT 71  
|||  
Db 14 AAGCTGGTGTCTT 2

```

RESULT 68
US-08-887-480-26/c
; Sequence 26, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs

```

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
; DESCRIPTION: Oligonucleotide primer JB443  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-887-480-26

Query Match 12.7%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 51;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCTGGG 19  
Db 13 AGACGGCTCCG 1

RESULT 69  
US-08-485-689-62/c  
; Sequence 62, Application US/08485689  
; Patent No. 5856188  
; GENERAL INFORMATION:  
; APPLICANT: Hampel, Arnold E.  
; APPLICANT: Tritz, Richard H.  
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States Of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,689  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 43863-CLX/JPW/KJP  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-278-0526  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA (genomic)  
US-08-485-689-62

Query Match 12.7%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 51;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAACAAGACGGCC 14  
Db 14 AAACAGGACGGTC 2

RESULT 70  
US-08-476-021A-62/c  
; Sequence 62, Application US/08476021A  
; Patent No. 5858785  
; GENERAL INFORMATION:  
; APPLICANT: Hampel, Arnold E.  
; APPLICANT: Tritz, Richard H.  
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States Of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,608B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678

; APPLICANT: Hampel, Arnold E.  
; APPLICANT: Tritz, Richard H.  
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States Of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,021A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 43863-DZ/JPW/KJP  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-278-0526  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA (genomic)  
US-08-476-021A-62

Query Match 12.7%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 51;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAACAAGACGGCC 14  
Db 14 AAACAGGACGGTC 2

RESULT 71  
US-08-478-608B-62/c  
; Sequence 62, Application US/08478608B  
; Patent No. 5869339  
; GENERAL INFORMATION:  
; APPLICANT: Hampel, Arnold E.  
; APPLICANT: Tritz, Richard H.  
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States Of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,608B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678

Query Match 12.7%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 51;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAACAAGACGGCC 14  
Db 14 AAACAGGACGGTC 2

RESULT 70  
US-08-476-021A-62/c  
; Sequence 62, Application US/08476021A  
; Patent No. 5858785  
; GENERAL INFORMATION:  
; APPLICANT: Hampel, Arnold E.  
; APPLICANT: Tritz, Richard H.  
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States Of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,608B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 43863-C1Z/JPW/KJP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-278-0400  
 TELEFAX: 212-278-0526  
 INFORMATION FOR SEQ ID NO: 62:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: RNA (genomic)  
 US-08-478-608B-62

Query Match 12.7%; Score 9.8; DB 1; Length 14;  
 Best Local Similarity 84.6%; Pred. No. 51;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAACAGACGGCC 14  
 Db 14 AAACAGACGGCT 2

## RESULT 72

US-08-722-187-26/c  
 Sequence 26, Application US/08722187  
 Patent No. 5955274  
 GENERAL INFORMATION:

APPLICANT: Ligon, James M  
 APPLICANT: Beck, James J  
 TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
 TITLE OF INVENTION: Polymerase Chain Reaction  
 NUMBER OF SEQUENCES: 86  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ciba-Geigy Corporation  
 STREET: 7 Skyline Drive  
 CITY: Hawthorne  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10532

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/722,187  
 FILING DATE:

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/233,608  
 FILING DATE: 04-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Walsh, Andrea C.  
 REGISTRATION NUMBER: 34,988  
 REFERENCE/DOCKET NUMBER: CGC 1739  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-541-8666  
 TELEFAX: 919-541-8689  
 INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Other nucleic acid  
 DESCRIPTION: Oligonucleotide primer JB443  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-722-187-26

Query Match 12.7%; Score 9.8; DB 1; Length 14;  
 Best Local Similarity 84.6%; Pred. No. 51;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGGG 19  
 Db 13 AGACGGCCTCGG 1

## RESULT 73

US-08-910-408-49/c  
 Sequence 49, Application US/08910408  
 Patent No. 5972704  
 GENERAL INFORMATION:

APPLICANT: Kenneth G. Draper  
 APPLICANT: Bharat Chowira  
 APPLICANT: James McSwiggen  
 APPLICANT: Dan T. Stinchcomb  
 APPLICANT: James D. Thompson  
 TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING  
 TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS  
 TITLE OF INVENTION: REPLICATION  
 NUMBER OF SEQUENCES: 232  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/910,408  
 FILING DATE:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/271,880  
 FILING DATE: July 7, 1994  
 APPLICATION NUMBER: 08/103,243  
 FILING DATE: August 6, 1993  
 APPLICATION NUMBER: 07/882,886  
 FILING DATE: May 14, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 206/116  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 49:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-910-408-49

Query Match 12.7%; Score 9.8; DB 1; Length 14;  
 Best Local Similarity 84.6%; Pred. No. 51;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 59 AAGCTGATGCTCT 71  
 Db 14 AAGCTGGTGTCT 2

## RESULT 74

US-08-985-162-1769  
 Sequence 1769, Application US/08985162  
 Patent No. 6057156

```

; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1769:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-1769

```

```

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 8 GACGGCCTGGGA 20
Db 2 GACGGCGGGGCA 14

```

```

RESULT 75
US-09-249-215-49/c
; Sequence 49, Application US/09249215
; Patent No. 6159692
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowrira
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; REPLICATION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700

```

```

; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,215
; FILING DATE: 12-Feb-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,408
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
; US-09-249-215-49

```

```

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 59 AAGCTGATGTCCT 71
Db 14 AAGCTGGTGTCT 2

```

```

RESULT 76
US-08-476-423A-62/c
; Sequence 62, Application US/08476423A
; Patent No. 6221661
; GENERAL INFORMATION:
; APPLICANT: Hampel, Arnold E.
; APPLICANT: Tritz, Richard H.
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States Of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,423A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.

```

```

; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 43863-C2/JPW/KJP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-278-0526
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-476-423A-62

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 AACACAGCGCC 14
Db  14 AACACAGCGTC 2

RESULT 77
US-09-135-020-99
; Sequence 99, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/135,020
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-020-99

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 AACACAGCGCC 14
Db  14 AACACAGCGTC 2

RESULT 77
US-09-135-020-99
; Sequence 99, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/135,020
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-020-99

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  34 TCCTCTGAGAGGT 46
Db  2 TCCTTTAAGAGGT 14

RESULT 79
US-09-373-845-19
; Sequence 19, Application US/09373845
; Patent No. 6316230
; GENERAL INFORMATION:
; APPLICANT: The Perkin-Elmer Corporation
; TITLE OF INVENTION: POLYMERASE EXTENSION AT 3' TERMINUS OF PNA-DNA CHIMERA
; FILE REFERENCE: 4468 US
; CURRENT APPLICATION NUMBER: US/09/373,845
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Bacterial
US-09-373-845-19

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  4 ACAAGACGGCTG 16
Db  1 ACACGACGGCCAG 13

RESULT 80
US-09-444-871-99
; Sequence 99, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,871
; CURRENT FILING DATE: 1999-11-22

```

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; EARLIER APPLICATION NUMBER: US 09/135,020
; EARLIER FILING DATE: 1998-08-17
; CURRENT APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-444-871-99

Query Match      12.7%   Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      34 TCCTCTGAGAGGT 46
Db      2 TCCTTTAAGAGGT 14

RESULT 81
US-09-081-646-24
; Sequence 24, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107, 74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-24

Query Match      12.7%   Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      65 ATGTCCTGTCAAG 77
Db      2 ATGTCCTATTAA 14

RESULT 82
US-09-597-735-99
; Sequence 99, Application US/09597735
; Patent No. 6420124
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE

; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,735
; CURRENT FILING DATE: 2000-06-19
; EARLIER APPLICATION NUMBER: 09/135,010
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-735-99

Query Match      12.7%   Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      34 TCCTCTGAGAGGT 46
Db      2 TCCTTTAAGAGGT 14

RESULT 83
US-09-444-295-99
; Sequence 99, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,295
; CURRENT FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-444-295-99

Query Match      12.7%   Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      34 TCCTCTGAGAGGT 46
Db      2 TCCTTTAAGAGGT 14

RESULT 84
US-09-597-732-99

```

```
; Sequence 99, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,732
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-732-99

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      34 TCCTCTGAGAGGT 46
      ||||| |||||
Db      2 TCCTTTAAGAGGT 14

RESULT 85
US-09-597-731-99
; Sequence 99, Application US/09597731
; Patent No. 6582913
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,731
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-731-99

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      34 TCCTCTGAGAGGT 46
      ||||| |||||
Db      2 TCCTTTAAGAGGT 14

RESULT 86
US-09-401-063-1769
; Sequence 1769, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OP DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: PatSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1769:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-401-063-1769

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 GACGGCTGGGGA 20
      ||||| |||||
Db      2 GACGGCTGGGGA 14

RESULT 87
PCT-US95-04712-26/c
; Sequence 26, Application PC/TUS9504712
```

GENERAL INFORMATION:  
APPLICANT: Ligon, James M  
APPLICANT: Beck, James J  
TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ciba-Geigy Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04712  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/233,608  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Walsh, Andrea C.  
REGISTRATION NUMBER: 34,988  
REFERENCE/DOCKET NUMBER: CGC 1739  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8666  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: Oligonucleotide primer JB443  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PCT-US95-04712-26

Query Match 12.7%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 51;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCCTGGG 19  
|||||  
Db 13 AGACGGCCTCCG 1

RESULT 88  
US-08-173-489C-331  
Sequence 331, Application US/08173489C  
Patent No. 5861244  
GENERAL INFORMATION:  
APPLICANT: WANG, C. -G.  
APPLICANT: HEPBURN, A. G.  
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
NUMBER OF SEQUENCES: 365  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
STREET: 510 EAST 73RD STREET,  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10021.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
COMPUTER: IBM PC/XT/AT

OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (attorney) (212) 708-1880  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 331:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
DESCRIPTION: 16s rRNA gene from Neisseria  
DESCRIPTION: gonorrhoeae (Accession # X07714) nucleotides  
DESCRIPTION: 189 to 199  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: Neisseria gonorrhoeae  
STRAIN: NCTC 83785  
PUBLICATION INFORMATION:  
AUTHORS: Rossau, R. Heyndrickx, L. van  
AUTHORS: Heuvelswyn, H.  
TITLE: Nucleotide sequence of a 16s  
TITLE: ribosomal RNA gene from Neisseria gonorrhoeae  
JOURNAL: Nucleic Acids Research  
VOLUME: 16  
PAGES: 6227-6227  
DATE: 1988  
RELEVANT RESIDUES IN SEQ ID NO: 331 :FROM 1 TO 11  
US-08-173-489C-331

Query Match 12.2%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 48;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 40 GAGAGGTAAG 50  
|||||  
Db 1 GAGAGGGAAAG 11

RESULT 89  
US-09-940-244-415  
Sequence 415, Application US/09940244  
Patent No. 6692917  
GENERAL INFORMATION:  
APPLICANT: Neri, Bruce P.  
APPLICANT: Hall, Jeff G.  
APPLICANT: Lyamichov, Victor  
APPLICANT: Smith, Lloyd M.  
TITLE OF INVENTION: Reactions on Dendrimers  
FILE REFERENCE: FORS-06478  
CURRENT APPLICATION NUMBER: US/09/940,244  
CURRENT FILING DATE: 2002-05-06  
NUMBER OF SEQ ID NOS: 422  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 415  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic



```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)...(4)
; OTHER INFORMATION: The residue at this position is linked to a spacer bearing a Cy3
; OTHER INFORMATION: dye.
US-09-940-244-415

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Query Match      12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 52;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 31 GAGTCCTCTGA 41
Db 1 GAGTCCTGTGA 11

```

```

RESULT 90
US-08-738-944-39
Sequence 39, Application US/08738944
Patent No. 5783431
GENERAL INFORMATION:
APPLICANT: Peterson, et al.
TITLE OF INVENTION: METHODS FOR GENERATING AND
SCREENING NOVEL METABOLIC PATHWAYS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
APPLICATION NUMBER: US/08/738,944
FILING DATE: 24-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/639,255
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8757-007
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Other
LOCATION: 5...6
OTHER INFORMATION: pDBLET Vector
US-08-738-944-39

```

```

Query Match      12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 50 GAGCCAGCGAA 60
Db 3 GAGCCAGCTAA 13

```

```

RESULT 91
US-08-468-037A-26/c
Sequence 26, Application US/08468037A
Patent No. 5859221
GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
APPLICANT: A. Kawasaki
TITLE OF INVENTION: 2'-Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859221ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,037A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 835,932
FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-037A-26

```

```

Query Match      12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 7 AGACGGCCTGG 17
Db 12 AAACGGCCTGG 2

```

```

RESULT 92
US-08-471-973A-26/c
Sequence 26, Application US/08471973A
Patent No. 5872232
GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
APPLICANT: Andrew Kawasaki
TITLE OF INVENTION: Sugar Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5872232ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

```
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,973A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 835,932
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-973A-26

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGACGGCCTGG 17
Db 12 AAACGGCCTGG 2

RESULT 94
US-09-263-352-30
; Sequence 30, Application US/09263352
; Patent No. 6242211
; GENERAL INFORMATION:
; APPLICANT: Brian, P.
; TITLE OF INVENTION: METHODS FOR GENERATING AND SCREENING NOVEL METABOLIC
; FILE REFERENCE: 8757-010
; CURRENT APPLICATION NUMBER: US/09/263,352
; CURRENT FILING DATE: 1999-03-05
; EARLIER APPLICATION NUMBER: 08/986,186
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
; US-09-263-352-30

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAA 60
Db 3 GAGCCAGCTAA 13

RESULT 95
US-08-936-166-6/c
; Sequence 6, Application US/08936166A
; Patent No. 6307040
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Sugar Modified Oligonucleotides That Detect And
; FILE REFERENCE: ISIS2708
; CURRENT APPLICATION NUMBER: US/08/936,166A
; CURRENT FILING DATE: 1997-09-23
; EARLIER APPLICATION NUMBER: 07/835,932
; EARLIER FILING DATE: 1992-03-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleoside
; OTHER INFORMATION: having a modified sugar moiety
; US-08-936-166-6

Query Match 12.2%; Score 9.4; DB 1; Length 13;
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Best Local Similarity 90.9%; Pred. No. 55;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGG 17  
| | | | | | | |  
Db 12 AAACGGCCTGG 2

RESULT 96  
US-09-135-202-26/c  
; Sequence 26, Application US/09135202  
; Patent No. 6399754  
; GENERAL INFORMATION:  
; APPLICANT: Phillip Dan Cook  
; APPLICANT: Andrew Kawasaki  
; TITLE OF INVENTION: Sugar Modified Oligonucleotides  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6399754ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 720 Kb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/135,202  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/471,973  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Joseph Lucci  
; REGISTRATION NUMBER: 33,307  
; REFERENCE/DOCKET NUMBER: ISIS-2005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-135-202-26

Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 55;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGG 17  
| | | | | | | |  
Db 12 AAACGGCCTGG 2

RESULT 97  
US-09-474-432B-141  
; Sequence 141, Application US/09474432B  
; Patent No. 6528640  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Beigelman, Leo  
; APPLICANT: Burgin, Alex  
; APPLICANT: Beaudry, Amber  
; APPLICANT: Karpelesky, Alex  
; APPLICANT: Adamic, Jasenka  
; APPLICANT: Sweedler, David  
; APPLICANT: Zinnen, Shawn

; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot  
; FILE REFERENCE: MH000-831-B (247/276)  
; CURRENT APPLICATION NUMBER: US/09/474,432B  
; CURRENT FILING DATE: 1999-12-19  
; PRIOR APPLICATION NUMBER: US 60/064,866  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: US 60/084,727  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: US 09/186,675  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: US 09/301,511  
; PRIOR FILING DATE: 1999-04-28  
; NUMBER OF SEQ ID NOS: 1526  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 141  
; LENGTH: 13  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-474-432B-141

Query Match 12.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 55;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGC 57  
| | | | | | | |  
Db 2 AGAGAGCCAGC 12

RESULT 98  
US-09-389-283-26/c  
; Sequence 26, Application US/09389283  
; Patent No. 6531584  
; GENERAL INFORMATION:  
; APPLICANT: Phillip Dan Cook  
; APPLICANT: A. Kawasaki  
; TITLE OF INVENTION: 2'-Modified Oligonucleotides  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6531584ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 720 Kb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/389,283  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/035,357  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Joseph Lucci  
; REGISTRATION NUMBER: 33,307  
; REFERENCE/DOCKET NUMBER: ISIS-2004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-389-283-26

Query Match 12.2%; Score 9.4; DB 1; Length 13;

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Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGACGGCCTGG 17
Db 12 AAACGGCCTGG 2

RESULT 99
US-09-476-387-141
; Sequence 141, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 141
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-141

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGC 57
Db 2 AGAGAGCCAGC 12

RESULT 100
US-10-042-819-8/c
; Sequence 8, Application US/10042819
; Patent No. 6897025
; GENERAL INFORMATION:
; APPLICANT: Perlegen Sciences, Inc.
; APPLICANT: Cox, David R
; APPLICANT: Margus, Bradley A
; TITLE OF INVENTION: GENETIC ANALYSIS SYSTEM AND METHODS
; FILE REFERENCE: 1016N1
; CURRENT APPLICATION NUMBER: US/10/042,819
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL SEQUENCE
US-10-042-819-8
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Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCAG 56
Db 12 TAAAGAGTCAG 2

Search completed: April 19, 2006, 16:10:20
Job time : 0.001 secs
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DR WPI; 2003-140495/13.
XX
PT New compound that hybridizes with and inhibits the expression of
PT Phospholipase A2, group IIA, useful for preparing a composition for
PT treating or preventing inflammation, cancer, psoriasis or diabetes.
XX
PS Claim 3; Page 86; 135pp; English.
XX
CC The present invention describes a compound (I) comprising 8-50
CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,
CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
CC A2, group IIA (synovial), where the compound specifically hybridizes with
CC and inhibits the expression of phospholipase A2, group IIA (synovial).
CC Also described: (1) a composition comprising the compound and a carrier
CC or diluent; (2) a method of inhibiting the expression of phospholipase
CC A2, group IIA in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with phospholipase A2, group IIA
CC (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
CC antipsoriatic activities, and can be used in vaccines and in gene
CC therapy. The compound (I) can be used for preparing a composition for
CC treating or preventing inflammation, cancer, psoriasis or diabetes. The
CC present sequence represents a human phospholipase A2 group IIA (synovial)
CC chimeric phosphorothioate antisense oligonucleotide, which is used in an
CC example from the present invention
XX
SQ Sequence .20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 CTCGAGAGGTAAGAGCCA 55
DB 20 CTCGAGAGGTAAGAGCCA 1

RESULT 7
ID ACC46925/c
XX ACC46925;
XX
XX 05-JUN-2003 (first entry)
XX
DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:22.
XX
KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
KW psoriasis; diabetes; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN WO200297133-A1.
XX
XX
PD 05-DEC-2002.
XX
XX 21-MAY-2002; 2002WO-US016135.
XX

```

```

XX 25-MAY-2001; 2001US-00865866.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Wyatt JR;
XX WPI; 2003-140495/13.
XX
XX New compound that hybridizes with and inhibits the expression of
XX phospholipase A2, group IIA, useful for preparing a composition for
XX treating or preventing inflammation, cancer, psoriasis or diabetes.
XX
XX Claim 3; Page 86; 135pp; English.
XX
XX The present invention describes a compound (I) comprising 8-50
XX nucleobases which is targeted to a 5' untranslated region (UTR), coding,
XX 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
XX A2, group IIA (synovial), where the compound specifically hybridizes with
XX and inhibits the expression of phospholipase A2, group IIA (synovial).
XX Also described: (1) a composition comprising the compound and a carrier
XX or diluent; (2) a method of inhibiting the expression of phospholipase
XX A2, group IIA in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with phospholipase A2, group IIA
XX (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
XX antipsoriatic activities, and can be used in vaccines and in gene
XX therapy. The compound (I) can be used for preparing a composition for
XX treating or preventing inflammation, cancer, psoriasis or diabetes. The
XX present sequence represents a human phospholipase A2 group IIA (synovial)
XX chimeric phosphorothioate antisense oligonucleotide, which is used in an
XX example from the present invention
XX
SQ Sequence .20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTCCTCTGAGAGGTAAGAG 52
DB 20 GTCCTCTGAGAGGTAAGAG 1

RESULT 8
ID ACC46922/c
XX ACC46922 standard; DNA; 20 BP.
XX
XX ACC46922;
XX
XX 05-JUN-2003 (first entry)
XX
DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:19.
XX
KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
KW psoriasis; diabetes; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
XX

```

CC or diluent; (2) a method of inhibiting the expression of phospholipase  
 CC A2, group IIA in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with phospholipase A2, group IIA  
 CC (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and  
 CC antipsoriatic activities, and can be used in vaccines and in gene  
 CC therapy. The compound (I) can be used for preparing a composition for  
 CC treating or preventing inflammation, cancer, psoriasis or diabetes. The  
 CC present sequence represents a human phospholipase A2 group IIA (synovial)  
 CC chimeric phosphorothioate antisense oligonucleotide, which is used in an  
 CC example from the present invention

XX Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 26.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGTCCTGTCAG 77  
 |||||  
 Db 20 GAAGCTGATGTCCTGTCAG 1

RESULT 5  
 ID ACC46927/c  
 XX ACC46927 standard; DNA; 20 BP.

AC ACC46927;

XX 05-JUN-2003 (first entry)

DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:24.

XX Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;  
 KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;  
 KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;  
 KW psoriasis; diabetes; ss.

OS Homo sapiens.

OS Synthetic.

Key	Location/Qualifiers
modified_base	1..20
	/*tag= a
	/mod_base= OTHER
	/note= "phosphorothioate backbone"
modified_base	1..5
	/*tag= b
	/mod_base= OTHER
	/note= "2'-O-methoxyethyl (2'-MOE) gapmer"
modified_base	16..20
	/*tag= C
	/mod_base= OTHER
	/note= "2'-O-methoxyethyl (2'-MOE) gapmer"

WO200297133-A1.

XX 05-DEC-2002.

XX 21-MAY-2002; 2002WO-US016135.

XX 25-MAY-2001; 2001US-00865866.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Wyatt JR;

XX WPI; 2003-140495/13.

XX New compound that hybridizes with and inhibits the expression of  
 PT Phospholipase A2, group IIA, useful for preparing a composition for  
 PT treating or preventing inflammation, cancer, psoriasis or diabetes.

XX Example 15; Page 86; 135pp; English.

XX The present invention describes a compound (I) comprising 8-50  
 CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,  
 CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase  
 CC A2, group IIA (synovial), where the compound specifically hybridizes with  
 CC and inhibits the expression of phospholipase A2, group IIA (synovial).  
 CC Also described: (1) a composition comprising the compound and a carrier  
 CC or diluent; (2) a method of inhibiting the expression of phospholipase  
 CC A2, group IIA in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with phospholipase A2, group IIA  
 CC (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and  
 CC antipsoriatic activities, and can be used in vaccines and in gene  
 CC therapy. The compound (I) can be used for preparing a composition for  
 CC treating or preventing inflammation, cancer, psoriasis or diabetes. The  
 CC present sequence represents a human phospholipase A2 group IIA (synovial)  
 CC chimeric phosphorothioate antisense oligonucleotide, which is used in an  
 CC example from the present invention

XX Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 26.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AGAGGTAAGAGCCAGCGAA 60  
 |||||  
 Db 20 AGAGGTAAGAGCCAGCGAA 1

RESULT 6

ID ACC46926/c

XX ACC46926 standard; DNA; 20 BP.

AC ACC46926;

XX 05-JUN-2003 (first entry)

DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:23.

XX Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;  
 KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;  
 KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;  
 KW psoriasis; diabetes; ss.

OS Homo sapiens.

OS Synthetic.

Key	Location/Qualifiers
modified_base	1..20
	/*tag= a
	/mod_base= OTHER
	/note= "phosphorothioate backbone"
modified_base	1..5
	/*tag= b
	/mod_base= OTHER
	/note= "2'-O-methoxyethyl (2'-MOE) gapmer"
modified_base	16..20
	/*tag= C
	/mod_base= OTHER
	/note= "2'-O-methoxyethyl (2'-MOE) gapmer"

WO200297133-A1.

XX 05-DEC-2002.

XX 21-MAY-2002; 2002WO-US016135.

XX 25-MAY-2001; 2001US-00865866.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Wyatt JR;

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FT      /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
PN      WO200297133-A1.
XX
XX      05-DEC-2002.
XX
XX      21-MAY-2002; 2002WO-US016135.
XX
XX      25-MAY-2001; 2001US-00865866.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Bennett CF, Wyatt JR;
XX
XX      WPI; 2003-140495/13.
XX
XX      New compound that hybridizes with and inhibits the expression of
XX      phospholipase A2, group IIA, useful for preparing a composition for
XX      treating or preventing inflammation, cancer, psoriasis or diabetes.
XX
XX      Claim 3; Page 86; 135pp; English.
XX
XX      The present invention describes a compound (I) comprising 8-50
XX      nucleobases which is targeted to a 5' untranslated region (UTR), coding,
XX      3' UTR or intron region of a nucleic acid molecule encoding phospholipase
XX      A2, group IIA (synovial), where the compound specifically hybridises with
XX      and inhibits the expression of phospholipase A2, group IIA (synovial).
XX      Also described: (1) a composition comprising the compound and a carrier
XX      or diluent; (2) a method of inhibiting the expression of phospholipase
XX      A2, group IIA in cells or tissues; and (3) a method of treating an animal
XX      having a disease or condition associated with phospholipase A2, group IIA
XX      (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
XX      antipsoriatic activities, and can be used in vaccines and in gene
XX      therapy. The compound (I) can be used for preparing a composition for
XX      treating or preventing inflammation, cancer, psoriasis or diabetes. The
XX      present sequence represents a human phospholipase A2 group IIA (synovial)
XX      chimeric phosphorothioate antisense oligonucleotide, which is used in an
XX      example from the present invention
XX
XX      Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX      Query Match      26.0%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 6.7;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 CAAACAGACGCGCTGGGA 20
DB      |||||
        20 CAAACAGACGCGCTGGGA 1

RESULT 9
ACC46924/c
ID      ACC46924 standard; DNA; 20 BP.
XX
XX      ACC46924;
XX
XX      05-JUN-2003 (first entry)
XX
XX      Human phospholipase A2 antisense oligonucleotide SEQ ID NO:21.
XX
XX      Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
XX      phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
XX      antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
XX      psoriasis; diabetes; ss.
XX
XX      Homo sapiens.
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      modified_base 1..20
XX      /tag= a
XX      /mod_base= OTHER
XX      /note= "phosphorothioate backbone"

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FT      modified_base 1..5
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
XX      modified_base 16..20
XX      /tag= c
XX      /mod_base= OTHER
XX      /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
XX      WO200297133-A1.
XX
XX      05-DEC-2002.
XX
XX      21-MAY-2002; 2002WO-US016135.
XX
XX      25-MAY-2001; 2001US-00865866.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Bennett CF, Wyatt JR;
XX
XX      WPI; 2003-140495/13.
XX
XX      New compound that hybridizes with and inhibits the expression of
XX      phospholipase A2, group IIA, useful for preparing a composition for
XX      treating or preventing inflammation, cancer, psoriasis or diabetes.
XX
XX      Claim 3; Page 86; 135pp; English.
XX
XX      The present invention describes a compound (I) comprising 8-50
XX      nucleobases which is targeted to a 5' untranslated region (UTR), coding,
XX      3' UTR or intron region of a nucleic acid molecule encoding phospholipase
XX      A2, group IIA (synovial), where the compound specifically hybridises with
XX      and inhibits the expression of phospholipase A2, group IIA (synovial).
XX      Also described: (1) a composition comprising the compound and a carrier
XX      or diluent; (2) a method of inhibiting the expression of phospholipase
XX      A2, group IIA in cells or tissues; and (3) a method of treating an animal
XX      having a disease or condition associated with phospholipase A2, group IIA
XX      (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
XX      antipsoriatic activities, and can be used in vaccines and in gene
XX      therapy. The compound (I) can be used for preparing a composition for
XX      treating or preventing inflammation, cancer, psoriasis or diabetes. The
XX      present sequence represents a human phospholipase A2 group IIA (synovial)
XX      chimeric phosphorothioate antisense oligonucleotide, which is used in an
XX      example from the present invention
XX
XX      Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX      Query Match      26.0%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 6.7;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      23 CAACTCTGGAGTCTCTGAG 42
DB      |||||
        20 CAACTCTGGAGTCTCTGAG 1

RESULT 10
ACC46923/c
ID      ACC46923 standard; DNA; 20 BP.
XX
XX      ACC46923;
XX
XX      05-JUN-2003 (first entry)
XX
XX      Human phospholipase A2 antisense oligonucleotide SEQ ID NO:20.
XX
XX      Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
XX      phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
XX      antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
XX      psoriasis; diabetes; ss.
XX
XX      Homo sapiens.

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OS Synthetic.
XX Key Location/Qualifiers
PH modified_base 1..20
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16..20
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX WO200297133-A1.
PN XX
XX 05-DEC-2002.
XX
XX 21-MAY-2002; 2002WO-US016135.
XX
XX 25-MAY-2001; 2001US-00865866.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Wyatt JR;
XX WPI; 2003-140495/13.
XX
XX New compound that hybridizes with and inhibits the expression of
XX phospholipase A2, group IIA, useful for preparing a composition for
XX treating or preventing inflammation, cancer, psoriasis or diabetes.
XX
XX Claim 3; Page 86; 135pp; English.
XX
XX The present invention describes a compound (I) comprising 8-50
XX nucleobases which is targeted to a 5' untranslated region (UTR), coding,
XX 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
XX A2, group IIA (synovial), where the compound specifically hybridises with
XX and inhibits the expression of phospholipase A2, group IIA (synovial).
XX Also described: (1) a composition comprising the compound and a carrier
XX or diluent; (2) a method of inhibiting the expression of phospholipase
XX A2, group IIA in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with phospholipase A2, group IIA
XX (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
XX antiproliferative activities, and can be used in vaccines and in gene
XX therapy. The compound (I) can be used for preparing a composition for
XX treating or preventing inflammation, cancer, psoriasis or diabetes. The
XX present sequence represents a human phospholipase A2 group IIA (synovial)
XX chimeric phosphorothioate antisense oligonucleotide, which is used in an
XX example from the present invention
XX
XX Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 GCCTGGGGATACAACTCTGG 31
DB 20 GCCTGGGGATACAACTCTGG 1
RESULT 11
ACLA45000/c
ID ACL45000 standard; RNA; 21 BP.
XX
XX ACL45000;
XX
XX 24-MAR-2005 (first entry)
XX
XX CDH6 siRNA antisense sequence, SEQ ID 6072.
XX
XX Synthetic.
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX short interfering RNA; gene silencing.
XX
XX Synthetic.
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell
XX activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 6072; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPRS4, HAVCR1, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 3 A; 6 C; 5 G; 0 T; 7 U; 0 Other;
Query Match 23.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 48 AAGAGCCAGCGAGCTGATGT 68
DB 21 AAAAGCCAGCGAGCTGATGT 1
RESULT 12
ACLA4998
ID ACL4998 standard; DNA; 21 BP.
XX
XX ACL4998;
XX
XX 24-MAR-2005 (first entry)
XX
XX CDH6 target oligonucleotide, SEQ ID 6070.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX

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PP 19-MAY-2004; 2004WO-US015645.
XX
PR 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell
XX activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 6070; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX target oligonucleotide from one such CRTP for which short interfering
XX RNAs (siRNA) were produced. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 6 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 21.8%; Score 16.8; DB 1; Length 21;
XX Best Local Similarity 90.0%; Pred. No. 23;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 49 AGAGCCAGCGAGCTGATGT 68
DB 2 AAAGCCAGCGAGCTGATGT 21
XX
RESULT 13
ACL44494
XX ACL44494 standard; DNA; 21 BP.
XX
XX ACL44494;
XX
XX 24-MAR-2005 (first entry)
XX
XX CDH6 target oligonucleotide, SEQ ID 5566.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
PP 19-MAY-2004; 2004WO-US015645.
XX
PR 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX Claim 3; SEQ ID NO 5566; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX target oligonucleotide from one such CRTP for which short interfering
XX RNAs (siRNA) were produced. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 21.8%; Score 16.8; DB 1; Length 21;
XX Best Local Similarity 90.0%; Pred. No. 23;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 49 AGAGCCAGCGAGCTGATGT 68
DB 1 AAAGCCAGCGAGCTGATGT 20
XX
RESULT 14
ACL44496/c
XX ACL44496 standard; RNA; 21 BP.
XX
XX ACL44496;
XX
XX 24-MAR-2005 (first entry)
XX
XX CDH6 siRNA antisense sequence, SEQ ID 5568.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX short interfering RNA; gene silencing.
XX
XX Synthetic.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell
XX activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 5568; 113pp; English.
XX

```



Query Match 21.3%; Score 16.4; DB 1; Length 21;  
 Best Local Similarity 94.4%; Pred. No. 27;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 51 AGCCAGCGAGCTGATGT 68  
 |||||  
 DB 2 AGCCAGCGAGCTGATGT 19

## RESULT 17

ACL44499/c  
 ID ACL44499 standard; RNA; 21 BP.

AC ACL44499;

DT 24-MAR-2005 (first entry)

DE CDH6 siRNA antisense sequence, SEQ ID 5571.

XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;  
 KW short interfering RNA; gene silencing.

XX Synthetic.

PN WO2005001092-A2.

XX 06-JAN-2005.

XX 19-MAY-2004; 2004WO-US015645.

XX 20-MAY-2003; 2003US-0471729P.

XX (AMHP ) WYETH.

XX Be X, Wei L, Slonim DK, Howes SH;

XX WPI; 2005-075568/08.

XX Pharmaceutical composition comprising an agent capable of modulating an  
 PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell  
 PT activated by the polypeptide or antibody, and a carrier, useful for  
 PT treating cancer.

XX Claim 3; SEQ ID NO 5571; 113pp; English.

XX The present invention relates to a novel pharmaceutical composition  
 CC comprising: (a) an agent capable of modulating an expression level or  
 CC protein activity of a cancer-related transmembrane protein (CRTP) or gene  
 CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
 CC (b) a carrier. The pharmaceutical composition may also comprise a  
 CC polynucleotide capable of inhibiting or decreasing the expression of the  
 CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
 CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
 CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
 CC pharmaceutical composition is useful for treating cancer, e.g. colon  
 CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
 CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
 CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 21 BP; 3 A; 8 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 21.3%; Score 16.4; DB 1; Length 21;  
 Best Local Similarity 94.4%; Pred. No. 27;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 51 AGCCAGCGAGCTGATGT 68  
 |||||  
 DB 20 AGCCAGCGAGCTGATGT 3

RESULT 18  
 ACL44999  
 ID ACL44999 standard; RNA; 21 BP.

XX ACL44999;

DT 24-MAR-2005 (first entry)

XX CDH6 siRNA sense sequence, SEQ ID 6071.

XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;  
 KW short interfering RNA; gene silencing.

XX Synthetic.

PN WO2005001092-A2.

XX 06-JAN-2005.

XX 19-MAY-2004; 2004WO-US015645.

XX 20-MAY-2003; 2003US-0471729P.

XX (AMHP ) WYETH.

XX Be X, Wei L, Slonim DK, Howes SH;

XX WPI; 2005-075568/08.

XX Pharmaceutical composition comprising an agent capable of modulating an  
 PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell  
 PT activated by the polypeptide or antibody, and a carrier, useful for  
 PT treating cancer.

XX Claim 3; SEQ ID NO 6071; 113pp; English.

XX The present invention relates to a novel pharmaceutical composition  
 CC comprising: (a) an agent capable of modulating an expression level or  
 CC protein activity of a cancer-related transmembrane protein (CRTP) or gene  
 CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
 CC (b) a carrier. The pharmaceutical composition may also comprise a  
 CC polynucleotide capable of inhibiting or decreasing the expression of the  
 CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
 CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
 CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
 CC pharmaceutical composition is useful for treating cancer, e.g. colon  
 CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
 CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
 CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 21 BP; 5 A; 5 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 21.3%; Score 16.4; DB 1; Length 21;  
 Best Local Similarity 77.8%; Pred. No. 27;  
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 51 AGCCAGCGAGCTGATGT 68  
 |||||  
 DB 2 AGCCAGCGAGCTGATGT 19

## RESULT 19

AAT4824/c

ID AAT4824 standard; DNA; 20 BP.

XX AAT4824;

XX 16-SEP-1997 (first entry)

DE PLA2s exon 1 primer, AB4.  
 XX Polymerase chain reaction; PCR; amplify; primer; PLA2s; mutation; APC;  
 KW type II non-pancreatic phospholipase A2; microsatellite; colon cancer;  
 KW adenomatous polyposis coli; ss.  
 XX Synthetic.  
 XX WO9641003-A1.  
 XX 19-DEC-1996.  
 XX 06-JUN-1996; 96WO-US009009.  
 XX 07-JUN-1995; 95US-00484359.  
 XX (UYJE-) UNIV JEFFERSON THOMAS.  
 XX Buchberg AM, Siracusa LD, Chepenik KP;  
 PI WPI; 1997-052369/05.  
 DR Identifying an individual at an elevated risk of colon cancer - by  
 XX detecting mutation(s) in PLA2s gene.  
 XX Example 1; Page 16; 78pp; English.  
 XX The sequences given in AAT48821-34 are primers which were used to amplify  
 CC regions of the type II non-pancreatic phospholipase A2 (PLA2s) gene at  
 CC which mutations occur. These primers amplify regions upstream of the  
 CC first exon and exon one, around the microsatellite, and exons 2, 3, 4 and  
 CC 5 and the surrounding sequences. These primers may be used in the method  
 CC of the invention for identifying an individual at an elevated risk of  
 CC colon cancer. The method comprises: (a) isolating genetic material from a  
 CC tissue or body fluid sample from the individual; and (b) detecting a  
 CC PLA2s gene mutation which is indicative of the individual is at an  
 CC elevated risk of colon cancer; or (b') detecting the absence of PLA2s  
 CC protein or PLA2s enzyme activity in an isolated protein sample which is  
 CC indicative of the individual having an elevated risk of colon cancer. The  
 CC method allows individuals with the APC (adenomatous polyposis coli)  
 CC mutation to be identified. In the treatment of colon cancer, the patient  
 CC is administered a recombinant vector incorporated within a non-toxic  
 CC enteric microorganism which expresses and secretes PLA2s  
 XX  
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 20.8%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 62 CTGATGTCCTGTCAG 77  
 Db 20 CTGATGTCCTGTCAG 5  
 RESULT 20  
 AD297584  
 ID AD297584 standard; DNA; 21 BP.  
 XX  
 AC AD297584;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DE Canine SNP detection, forward PCR primer SEQ ID No:181.  
 XX animal breeding; genetic marker; SNP detection; allelic variation;  
 KW infection; diabetes; hypertension; atherosclerosis; autoimmune disease;  
 KW renal disease; neurological disease; PCR; primer; ss.  
 XX Canidae.  
 OS  
 XX WO2005040350-A2.  
 PN  
 XX

PD 06-MAY-2005.  
 XX 25-OCT-2004; 2004WO-US035231.  
 XX 24-OCT-2003; 2003US-0514180P.  
 PR 08-OCT-2004; 2004US-0617383P.  
 XX (MMIG-) MMI GENOMICS INC.  
 PA  
 PI Rosenfeld D, Kerr R, Hutton M, Denise S, Bates S, Fantin D;  
 XX WPI; 2005-333502/34.  
 DR Identifying animal genetic marker that influences trait for determining  
 XX parentage or to infer breed/line in e.g. canines involves analyzing  
 PT markers of genome-wide genetic marker map for association with genetic  
 PT trait.  
 XX  
 XX Claim 44; SEQ ID NO 181; 145pp; English.  
 PS  
 XX The invention relates to a method of identifying a companion animal  
 CC genetic marker that influences a phenotype or trait comprising analyzing  
 CC companion animal genetic markers of a genome-wide genetic marker map for  
 CC association with the genetic trait and identifying the companion animal  
 CC genetic marker that influences the trait. Also described are: (i) a high  
 CC throughput system for determining the nucleotide occurrences at a series  
 CC of companion animal SNPs comprising a hybridization medium containing a  
 CC series of oligonucleotides that bind at or near a genomic location of  
 CC each SNP of the series of companion animal SNPs, a mechanism for moving  
 CC the solid support or other hybridization medium, and a liquid handling  
 CC mechanism for applying a liquid to the series of oligonucleotides,  
 CC binding of oligonucleotide to a polynucleotide isolated from a genome is  
 CC affected by the nucleotide occurrence of the SNP; (ii) a kit for  
 CC determining nucleotide occurrences of canine SNPs, comprising an  
 CC oligonucleotide probe and/or primer/primer pair for identifying the  
 CC nucleotide occurrence of at least one canine SNP corresponding to the  
 CC first nucleotide or complement in the most 3' position of nucleotide  
 CC sequences given as SEQ ID Nos 1-101 in the specification; (iii) a  
 CC database comprising each SNP corresponding to the first nucleotide or  
 CC complement in the most 3' position of nucleotide sequences in SEQ ID Nos  
 CC 1-101; (iv) a computer-based method for identifying/infering a trait of  
 CC a canine test involving identifying from the obtained subject nucleic  
 CC acid sample at least one nucleotide occurrence of at least one SNP  
 CC corresponding to the first nucleotide, or complement its in the most 3'  
 CC position of nucleotide sequences in SEQ ID Nos 1-101, searching a  
 CC database comprising allele frequencies and retrieving information,  
 CC optionally storing the information in a memory location associated with a  
 CC user such that the information may be subsequently accessed and viewed by  
 CC the user, and identifying the trait of a canine subject; (v) an isolated  
 CC oligonucleotide comprising any one of the nucleotide sequences given as  
 CC SEQ ID Nos 306-407 in the specification, and further including one  
 CC additional nucleotide positioned proximal to the 3' end of each  
 CC oligonucleotide that specifically hybridizes to a nucleic acid sequence  
 CC derived from a canine subject, or a first nucleotide or its complement  
 CC with nucleotide sequences in SEQ ID Nos 1-101; (vi) an isolated SNP  
 CC corresponding to the first nucleotide or complement in the most 3'  
 CC position of any one of the nucleotide sequences in SEQ ID Nos 1-101;  
 CC (vii) a panel comprising at least one SNP corresponding to the first  
 CC nucleotide, or complement in the most 3' position of a nucleotide  
 CC sequence in SEQ ID Nos 1-101; (viii) generating a genome discovery map  
 CC involving selecting several SNP markers corresponding to the first  
 CC nucleotide or complement in the most 3' position of any one of nucleotide  
 CC sequence in SEQ ID Nos 1-101, each marker in the series separated by  
 CC 15000 bp, and generating the genome discovery map based upon the  
 CC selected markers; (ix) identifying the parentage of a canine test subject  
 CC involving obtaining a nucleic acid sample from the test subject by  
 CC identifying in the nucleic acid sample at least one SNP corresponding to  
 CC the first nucleotide or complement in the most 3' position of any one of  
 CC nucleotide sequence in SEQ ID Nos 1-101, determining the alleles to  
 CC corresponding to each SNP identified, and comparing the alleles to  
 CC putative parents of the test subject such that parents that do not  
 CC possess at least one allele in common with the test subject are excluded,  
 CC and (x) the use of a first primer selected from SEQ ID Nos 102-203, and a

CC second primer selected from SEQ ID Nos 204-305 in the method of the  
CC invention. The method is useful for identifying a companion animal  
CC genetic marker that influences a phenotype or trait and determine the  
CC parentage or to infer breed/line of a canine test subject, for  
CC identifying/infering a genetic trait (preferably resistant to disease or  
CC infection), susceptibility to infection, regulation of immune status and  
CC response to antigens, previous exposure to infection or parasites,  
CC bone/joint health, coat color/health, body mass, health of respiratory  
CC and digestive tissues, diabetes, hypertension, atherosclerosis,  
CC autoimmune disorders, kidney disease and neurological disease in  
CC companion animal (preferably dogs, cats, fish, reptiles, birds, horses,  
CC rabbits, hamsters, gerbils, mice or rats, especially dog). The  
CC methods/systems help for managing, selecting and breeding companion  
CC animals, maximizing individual potential performance and health, allowing  
CC predictive (predisposition) diagnostics, nutritional therapies and  
CC veterinary pharmaceutical therapeutics as applied to companion animals,  
CC and collect, record and store data by individual animal identification so  
CC that it is usable to improve future animals bred by animal owners and  
CC breeders. The methods/systems are also useful for assessing complex  
CC traits such as energy metabolism, aging and breed-specific traits to  
CC improve profits related to selling a companion animal, to manage, sort,  
CC and improve the genetics of a companion animal population by selecting  
CC and breeding of companion animal, to clone a companion animal with a  
CC specific genetic trait(s) or combination of SNP markers that predict a  
CC genetic trait, to track a companion animal or offspring, and to diagnose  
CC a health condition of a companion animal. This sequence represents a PCR  
CC primer used for the detection of canine SNPs.

XX  
SQ Sequence 21 BP; 6 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 20.5%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 33;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 39 TGAGAGCTTAAGGCCAGC 57  
Db 1 TGAGTGGTAATAGCCAGC 19

RESULT 21  
ACL44498  
ID ACL44498 standard; RNA; 21 BP.  
AC ACL44498;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
DE CDH6 siRNA sense sequence, SEQ ID 5570.  
XX  
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;  
KW short interfering RNA; gene silencing.  
XX  
XX Synthetic.  
XX  
XX W02005001092-A2.  
FN  
PD 06-JAN-2005.  
XX  
XX 19-MAY-2004; 2004WO-US015645.  
XX  
XX 20-MAY-2003; 2003US-0471729P.  
XX  
XX (AMHP ) WYETH.  
XX  
XX Be X, Wei L, Slonim DK, Howes SH;  
XX  
XX WPI; 2005-075568/08.  
XX  
XX Pharmaceutical composition comprising an agent capable of modulating an  
XX expression level or protein activity of a gene, e.g. ABC4, or a T cell  
XX activated by the polypeptide or antibody, and a carrier, useful for  
XX treating cancer.

PS Claim 3; SEQ ID NO 5570; 113pp; English.  
XX  
CC The present invention relates to a novel pharmaceutical composition  
CC comprising: (a) an agent capable of modulating an expression level or  
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene  
CC , an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
CC (b) a carrier. The pharmaceutical composition may also comprise a  
CC polynucleotide capable of inhibiting or decreasing the expression of the  
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
CC pharmaceutical composition is useful for treating cancer, e.g. colon  
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a  
CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pat\_sequences

XX  
SQ Sequence 21 BP; 3 A; 5 C; 8 G; 0 T; 5 U; 0 Other;

Query Match 20.0%; Score 15.4; DB 1; Length 21;  
Best Local Similarity 76.5%; Pred. No. 38;  
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 52 GCCAGCGAAGCTGATGT 68  
Db 1 GCCAGCGAGCGUGAUGU 17

RESULT 22  
ADD35279  
ID ADD35279 standard; DNA; 22 BP.  
XX  
AC ADD35279;  
XX  
XX 15-JAN-2004 (first entry)  
XX  
DE Human KIAA0172 exon 1 primer #14.  
XX  
XX human; KIAA0172; cancer; ss; PCR; primer.  
XX  
XX Homo sapiens.  
OS  
PN JP2002369696-A.  
XX  
PD 24-DEC-2002.  
XX  
PF 01-APR-2002; 2002JP-00099422.  
XX  
XX 30-MAR-2001; 2001JP-00101401.  
XX  
XX (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.  
PA (INFO-) INFO GENES CO LTD.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
XX  
XX WPI; 2003-495749/47.  
XX  
XX Human KIAA0172 gene encoding a sequence of 1194 amino acids, useful for  
PT diagnosis and treatment of cancer and for development of effective growth  
PT inhibitors of cancer cells.

Example 2; SEQ ID NO 15; 40pp; Japanese.

XX  
XX The invention relates to new human KIAA0172 gene. The KIAA0172 gene and  
CC polypeptide are useful for detection and treatment of cancer. The present  
CC sequence represents KIAA0172 associated primer.

SQ Sequence 22 BP; 5 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 20.0%; Score 15.4; DB 1; Length 22;  
Best Local Similarity 94.1%; Pred. No. 40;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



```

XX JN2001321190-A.
XX 20-NOV-2001.
XX 12-MAR-2001; 2001JP-00068285.
XX 10-MAR-2000; 2000JP-00066716.
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX WPI; 2002-144136/19.
XX Arraying genome clones.
XX Claim 4; Page 35; 528pp; Japanese.
XX The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in
XX multiwell plates numbered for discrimination are mixed in each of the
XX multiwell plates; (b) a primer designed based on the chromosome marker
XX sequence is added to the mixture to carry out an amplification reaction;
XX (c) a signal corresponding to the marker is detected from the resultant
XX amplified product to specify the discrimination Nos. of the multiwell
XX plates containing the clones having said marker sequence; (d) the order
XX of the markers is changed so that the same discrimination Nos. succeed to
XX the maximum in the specified discrimination Nos. to array the multiwell
XX plates; (e) the clones in the multiwell plates of the specified
XX discrimination Nos. are mixed respectively in each wells of longitudinal
XX and lateral directions; (f) the mixed clones are cultured and the
XX resultant cultures are amplified by using the above primer; (g) signals
XX are detected from the amplified products; (h) the clones in the multiwell
XX plates are specified from the detected result; and (i) the clones are
XX reconstituted as the positions on the chromosome and arrayed. The
XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
XX represent PCR primers for human chromosome 21q22.1, which are
XX specifically claimed for use in the present invention
XX
XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
XX
Query Match 19.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGACGAGCT 63
DB 18 TGAAGAGCCGACGAGCT 1

RESULT 26
AAD35822
ID AAD35822 standard; DNA; 21 BP.
XX
AC AAD35822;
XX
XX 26-JUL-2002 (first entry)
XX
DE RACE PCR primer #1, used for cloning human SU(FU) homologue.
XX
XX Human; Drosophila suppressor; human hedgehog-patched pathway; HH-PTC;
XX sonic hedgehog-patched pathway; SHH-PTC; intracellular signal;
XX split hand; split foot malformation type 3; SHFM3; wound healing;
XX neurodegenerative disease; testicular; cancer; gene therapy; cytotatic;
XX neuroprotective; rapid amplification of cDNA end; RACE; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO9932517-A1.
XX
XX 01-JUL-1999.
XX

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PF 18-DEC-1998; 98WO-SE002383.
XX
XX 19-DEC-1997; 97SE-00004788.
PR 26-JUN-1998; 98SE-00002293.
XX
XX (KARO-) KAROLINSKA INNOVATIONS AB.
XX
XX Toftgard R, Zaphiropoulos PG, Kogerman P, Grimm T;
XX WPI; 1999-405160/34.
XX
XX Human homolog of the Drosophila suppressor of fused gene useful in the
XX treatment of Split hand/Split foot Malformation Type 3.
XX
XX Example; Page 67; 82pp; English.
XX
XX The invention relates to proteins, polypeptides and nucleotides related
XX to the human homologue of the Drosophila suppressor of fused gene, which
XX is involved in the transduction of signals in the human hedgehog-patched
XX (HH-PTC) pathway. Protein molecule capable of eliciting an intracellular
XX signal in the HH-PTC pathway, its antibodies and pharmaceutical
XX compositions comprising them can be used as medicaments for the treatment
XX and/or prevention of split hand/split foot malformation type 3 (SHFM3).
XX The polynucleotides and polypeptides of the invention can be used to gain
XX an understanding of a signalling pathway that is central to normal
XX development and often disrupted in disease. This knowledge will be value
XX for therapeutic strategies involving modification of sonic hedgehog-
XX patched (SHH-PTC) signalling pathway. Potential areas include
XX tissue/wound healing, neurodegenerative diseases, testicular function and
XX cancer. The polynucleotides of the invention may also be used in gene
XX therapy methods. The present sequence is a rapid amplification of cDNA
XX ends (RACE) PCR primer used for cloning human SU(FU) homologue. This
XX sequence is used in the exemplification of the invention
XX
XX Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTGTCA 75
DB 1 GAAGCTGATGCTACTGCCA 18

RESULT 27
ADT92489
ID ADT92489 standard; DNA; 21 BP.
XX
XX ADT92489;
XX
XX 16-DEC-2004 (first entry)
XX
XX Human suppressor of fused (SU(FU)) primer seqid 3.
XX
XX cytotatic; neuroprotective; suppressor of fused; SU(FU);
XX signal transduction; patched receptor; hedgehog ligand;
XX hedgehog-patched pathway; HH-PTC pathway;
XX Split hand/Split foot Malformation Type 3; SHFM3; sonic hedgehog-patched;
XX SHH-PTC signal pathway; tissue healing; wound healing;
XX neurodegenerative disease; testicular function; cancer; gene therapy;
XX human; SU(FU); PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX US6448020-B1.
XX
XX 10-SEP-2002.
XX
XX 21-AUG-2000; 2000US-00581831.
XX
XX 19-DEC-1997; 97SE-00004788.
PR 26-JUN-1998; 98SE-00002293.
XX

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PR 18-DEC-1998; 98WO-SR002383.
XX (TOFT/) TOFTGARD R.
PA (ZAPH/) ZAPHIROPOULOS P G.
PA (KOG/) KOGERMAN P.
XX
XX Toftgard R, Zaphiropoulos PG, Kogerman P, Grimm T;
XX WPI; 1999-405160/34.
XX
XX Human homolog of the Drosophila suppressor of fused gene useful in the
XX treatment of Split hand/Split foot Malformation Type 3.
XX
XX Example; SEQ ID NO 3; 37pp; English.
XX
XX The invention describes novel human homologues to molecules associated
XX with the Drosophila suppressor of fused (SUFU) gene. These molecules are
XX implicated in the transduction of the signals that are elicited by the
XX interaction between the patched receptor and any one of the hedgehog
XX ligands. Also described are: an isolated protein molecule (I) capable of
XX eliciting an intracellular signal in the human hedgehog-patched (HH-PTC)
XX pathway and exhibiting a substantial similarity (especially about 80%),
XX the amino acid sequence is not given in the specification; an isolated
XX human DNA sequence (II) capable of involvement in eliciting an
XX intracellular signal in the HH-PTC pathway, the nucleotide sequence is
XX not given in the specification; a DNA sequence encoding the protein of
XX (I) or their variants; a vector comprising (II) or the DNA sequence (3);
XX an expression cassette comprising (II) or the DNA sequence (3); a cell
XX comprising the expression cassette of (5); an antibody that binds
XX specifically to (I); a recombinant cell expressing the antibody of (7); a
XX kit for the detection of a human suppressor of fused gene, comprising a
XX nucleic acid sequence capable of hybridising specifically with (II); and
XX a kit for the detection of a protein encoded by the human suppressor of
XX fused gene, comprising a container containing the antibody of (7). (I),
XX its antibodies and pharmaceutical compositions comprising them can be
XX used as medicaments for the treatment and/or prevention of Split
XX hand/Split foot Malformation Type 3 (SHFM3). The polynucleotides and
XX polypeptides can be used to gain an understanding of a signaling pathway
XX that is central to normal development and often disrupted in disease.
XX This knowledge will be value for therapeutic strategies involving
XX modification of sonic hedgehog-patched (SHH-PTC) signaling pathway.
XX Potential areas include tissue/wound healing, neurodegenerative diseases,
XX testicular function and cancer. The polynucleotide may also be used in
XX gene therapy methods. This sequence represents a primer used to isolate
XX DNA encoding human suppressor of fused (SUFUH).
XX
XX Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
SQ
Query Match 19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTGTCA 75
Db 1 GAAGCTGATGCTCTGTCA 18
|||||
|||||

RESULT 28
AD93548/c
ID AD93548 standard; RNA; 21 BP.
XX
XX AD93548;
AC
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Human MRCK2 siRNA sequence SeqID14.
DE
XX
XX human protein kinase; MCRK2;
XX myotonic dystrophy kinase-related Cdc42 binding kinase 2; 1q42;
XX chromosome 1; pkinase_C domain; DAG-PE; CNH domain;
XX cytoskeleton reorganisation; cytosstatic; antinflammatory;
XX antiarteriosclerotic; ophthalmological; antipsoriatic; antiasthmatic;
XX antiparkinsonian; antirheumatic; antiarthritic; neuroprotective;

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KW muscular-Gen; osteopathic; cardiovascular-Gen; immunosuppressive;
KW cerebroprotective; vasotropic; anticonvulsant; anti-HIV; MRCK2-modulator;
KW gene therapy; inflammation; cancer; arteriosclerosis; psoriasis; asthma;
KW Parkinson's disease; rheumatoid arthritis; spinal cord injury;
KW muscle condition; osteoporosis; graft versus host disease;
KW cardiovascular disorder; autoimmune disorder; retinal detachment; stroke;
KW epilepsy; ischaemia; reperfusion; breast cancer; ovarian cancer;
KW glioblastoma; non-Hodgkin's lymphoma; colorectal cancer;
KW non-small cell lung cancer; brain cancer; Kaposi's sarcoma;
KW pancreatic cancer; liver cancer; tumour; siRNA; short interfering RNA;
KW human; ss.
XX
XX Homo sapiens.
XX
XX WO2004033638-A2.
XX
XX 22-APR-2004.
XX
XX 07-OCT-2003; 2003WO-US031591.
XX
XX 07-OCT-2002; 2002US-0416257P.
XX
XX (AMHP ) WYETH.
XX (LIUW/) LIU W.
XX (WULW/) WU L.
XX
XX Liu W, Wu L;
XX
XX WPI; 2004-340908/31.
XX
XX New isolated polypeptide, useful for preventing or treating a myotonic
XX dystrophy kinase-related Cdc42 binding kinase 2 (MRCK2)-related disease
XX e.g., inflammation, cancer, arteriosclerosis, psoriasis, and Parkinson's
XX disease.
XX
XX Disclosure; SEQ ID NO 14; 242pp; English.
XX
XX This invention relates to a novel isolated human protein kinase, MCRK2.
XX The sequence shows homology to rat myotonic dystrophy kinase-related
XX Cdc42 binding kinase 2 (MRCK2). The gene encoding the novel kinase is
XX localised to human in locus 1q42 of human chromosome 1. The novel protein
XX kinase comprises multiple functional/structural domains that include a
XX kinase domain, a pkinase_C domain, a DAG-PE binding domain and a CNH
XX domain. The protein may function as a downstream effector of Cdc42 in
XX cytoskeleton reorganisation. The invention may be useful for the
XX production of cytostatic, antiinflammatory, antiarteriosclerotic,
XX ophthalmological, antipsoriatic, antiasthmatic, antiparkinsonian,
XX antirheumatic, antiarthritic, neuroprotective, muscular-Gen, osteopathic,
XX cardiovascular-Gen, immunosuppressive, cerebroprotective, vasotropic,
XX anticonvulsant or anti-HIV activity acting as myotonic dystrophy kinase-
XX related Cdc42 binding kinase 2 (MRCK2)-inhibitors or MRCK2-Modulator. In
XX addition, the disclosed sequences may be used for gene therapy. The
XX invention may be useful for preventing or treating an myotonic dystrophy
XX kinase-related Cdc42 binding kinase 2 (MRCK2)-related disease in a
XX subject such as inflammation, cancer, arteriosclerosis, psoriasis,
XX asthma, Parkinson's disease, rheumatoid arthritis, spinal cord injuries,
XX muscle conditions, osteoporosis, graft versus host disease,
XX cardiovascular disorders, autoimmune disorders, retinal detachment,
XX stroke, epilepsy, ischaemia/reperfusion, breast cancer, ovarian cancer,
XX glioblastoma, non-Hodgkin's lymphoma, colorectal cancer, non-small cell
XX lung cancer, brain cancer, Kaposi's sarcoma, pancreatic cancer, liver
XX cancer and other tumours. The MRCK2 and MRCK2 gene are useful as models
XX for the development of human therapeutic targets, aid in the
XX identification of therapeutic proteins, and serve as targets for the
XX development of human therapeutic agents that modulate kinase activity in
XX cells and tissues that express the kinase. The present sequence is that
XX of a short interfering RNA (siRNA) molecule which was designed to target
XX the human MRCK2 coding sequence and which is related to the invention.
XX
XX Sequence 21 BP; 5 A; 4 C; 5 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 19.2%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 47;

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 24 AACTCTGAGTCTCTGA 41
  ||| ||| ||| ||| ||| |||
Db 21 AAGTCTAGAGTCTCTGA 4

RESULT 29
ACL44492
ID ACL44492 standard; RNA; 21 BP.
AC ACL44492;
XX
XX
DT 24-MAR-2005 (first entry)
XX
XX CDH6 siRNA sense sequence, SEQ ID 5564.
DE
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX short interfering RNA; gene silencing.
XX Synthetic.
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
XX
XX Claim 3; SEQ ID NO 5564; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 6 A; 6 C; 5 G; 0 T; 4 U; 0 Other;
SQ

Query Match 19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 49 AGAGCCAGCGAGTGTAT 66
  ||| ||| ||| ||| |||
Db 3 AAAGCCAGCGAGCGTGAU 20

RESULT 30
ABN10034
```

```
ID XX ABN10034 standard; DNA; 17 BP.
AC AC
XX
XX ABN10034;
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10026.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234468P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 10026; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
```

Query Match 18.7%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 42;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAG 42  
 DB 2 TCTGGAGTCTCTGTG 17

RESULT 31  
 ABN10035  
 ID ABN10035 standard; DNA; 17 BP.  
 XX AC ABN10035;  
 XX DT 29-MAY-2002 (first entry)  
 XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10027.  
 XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX OS Homo sapiens.  
 XX PN WO200192524-A2.  
 XX PD 06-DEC-2001.  
 XX PF 25-MAY-2001; 2001WO-US016981.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PR 30-JAN-2001; 2001WO-US000661.  
 XX PR 30-JAN-2001; 2001WO-US000662.  
 XX PR 30-JAN-2001; 2001WO-US000663.  
 XX PR 30-JAN-2001; 2001WO-US000664.  
 XX PR 30-JAN-2001; 2001WO-US000665.  
 XX PR 30-JAN-2001; 2001WO-US000666.  
 XX PR 30-JAN-2001; 2001WO-US000667.  
 XX PR 30-JAN-2001; 2001WO-US000668.  
 XX PR 30-JAN-2001; 2001WO-US000669.  
 XX PR 30-JAN-2001; 2001WO-US000670.  
 XX PR 05-FEB-2001; 2001US-0266860P.  
 XX PA (ABOM-) AEOMICA INC.  
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 XX DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX PS Disclosure; SEQ ID NO 10027; 214pp; English.  
 XX CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The

CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence

XX SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
 Query Match 18.7%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 42;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAG 42  
 DB 1 TCTGGAGTCTCTGTG 16

RESULT 32  
 ACN73125  
 ID ACN73125 standard; DNA; 17 BP.  
 XX AC ACN73125;  
 XX DT 02-DEC-2004 (first entry)  
 XX DE Human GDMPLP-1 probe SEQ ID NO:10027.  
 XX KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX OS Homo sapiens.  
 XX PN US2004137589-A1.  
 XX PD 15-JUL-2004.  
 XX PF 26-NOV-2003; 2003US-00723361.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PR 30-JAN-2001; 2001WO-US000661.  
 XX PR 30-JAN-2001; 2001WO-US000662.  
 XX PR 30-JAN-2001; 2001WO-US000663.  
 XX PR 30-JAN-2001; 2001WO-US000664.  
 XX PR 30-JAN-2001; 2001WO-US000665.  
 XX PR 30-JAN-2001; 2001WO-US000666.  
 XX PR 30-JAN-2001; 2001WO-US000667.  
 XX PR 30-JAN-2001; 2001WO-US000668.  
 XX PR 30-JAN-2001; 2001WO-US000669.  
 XX PR 30-JAN-2001; 2001WO-US000670.  
 XX PR 05-FEB-2001; 2001US-0266860P.  
 XX PR 25-MAY-2001; 2001US-00866108.  
 XX PA (GUY/) GU Y.  
 XX PA (JIY/) JI Y.  
 XX PA (PENN/) PENN S G.  
 XX PA (HANZ/) HANZEL D K.  
 XX PA (RANK/) RANK D.  
 XX PA (CHEN/) CHEN W.  
 XX PA (SHAN/) SHANNON M E.  
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 XX WPI; 2004-533378/51.  
 XX DR Novel myosin-like protein-1, useful for treating or preventing disorder  
 XX associated with decreased expression or activity of human genome-derived  
 PT

PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 XX function.  
 XX  
 XX Disclosure; SEQ ID NO 10027; Opp; English.  
 XX  
 XX The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
 Query Match 18.7%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 42;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 27 TCTGGAGTCTCTCTGAG 42  
 |||||  
 DB 1 TCTGGAGTCTCTCTGTG 16  
 RESULT 33  
 ACN73124  
 ID ACN73124 standard; DNA; 17 BP.  
 XX  
 AC ACN73124;  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human GDMLP-1 probe SEQ ID NO:10026.  
 XX  
 KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;  
 KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004137589-A1.  
 XX  
 PD 15-JUL-2004.  
 XX  
 PF 26-NOV-2003; 2003US-00723361.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001WO-US00680P.  
 PR 25-MAY-2001; 2001US-00866108.  
 XX  
 XX (GUY/) GU Y.  
 PA (JIY/) JI Y.  
 PA (PENN/) PENN S G.  
 PA (HANZ/) HANZEL D K.  
 PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.

PA (SHAN/) SHANNON M E.  
 XX  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 XX WPI; 2004-533378/51.  
 XX  
 XX Novel myosin-like protein-1, useful for treating or preventing disorder  
 PT associated with decreased expression or activity of human genome-derived  
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 PT function.  
 XX  
 XX Disclosure; SEQ ID NO 10026; Opp; English.  
 XX  
 XX The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
 Query Match 18.7%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 42;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 27 TCTGGAGTCTCTCTGAG 42  
 |||||  
 DB 2 TCTGGAGTCTCTCTGTG 17  
 RESULT 34  
 AAZ31818/c  
 ID AAZ31818 standard; DNA; 18 BP.  
 XX  
 AC AAZ31818;  
 XX  
 DT 24-JAN-2000 (first entry)  
 XX  
 DE Human G-alpha-13 antisense inhibitor ISIS# 20767.  
 XX  
 KW G-alpha-13; human; inhibitor; cancer; antisense compound; therapy; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US5981732-A.  
 XX  
 PD 09-NOV-1999.  
 XX  
 PF 04-DEC-1998; 98US-00205860.  
 XX  
 PR 04-DEC-1998; 98US-00205860.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 XX Cowbert LM;  
 PI WPI; 1999-633376/54.  
 XX  
 DR Antisense compound inhibiting expression of human G-alpha-13.  
 XX  
 XX Claim 11; Col 39; 38pp; English.  
 XX  
 XX This sequence represents an antisense inhibitor of the invention, and  
 CC inhibits the expression of the human G-alpha-13 protein. The antisense  
 CC compounds of the invention are of 8 to 30 nucleobases in length, that  
 CC inhibits the expression of the human G-alpha-13. The antisense compound

CC is useful for treating an animal, particularly humans, having or being  
 CC prone to a disease or condition associated with the expression of G-alpha  
 CC -13, such as cancer

XX  
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 18.7%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 45;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 CCTGGGGATACAACTC 28  
 |||||  
 Db 17 CCTGGGGAGACAACTC 2

RESULT 35  
 ADK74660/c  
 ID ADK74660 standard; DNA; 20 BP.

XX AC ADK74660;  
 XX  
 DT 20-MAY-2004 (first entry)

XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1994.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
 KW diabetic neuropathy; arthritic pain; migraine headache;  
 KW infantile epilepsy; ataxia; ss.

XX Synthetic.

XX WO2004016754-A2.

XX 26-FEB-2004.

XX 14-AUG-2003; 2003WO-US025465.

PR 14-AUG-2002; 2002US-0403416P.

XX (PHAA ) PHARMACIA CORP.

XX Roberds SL;

XX WPI; 2004-203785/19.

XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT Nav1.3, useful for treating a disease or condition associated  
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 PT disorder, or ataxia.

XX Claim 4; SEQ ID NO 1994; 417pp; English.

XX The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 18.4%; Score 14.2; DB 1; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 55;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 36 CTCCTGAGAGCTAAAGACC 54  
 |||||  
 Db 20 CTCCTGAGAGCTAAAGACC 2

RESULT 36

ADK73231/c

ID ADK73231 standard; DNA; 20 BP.

XX ADK73231;

AC ADK73231;

DT 20-MAY-2004 (first entry)

XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #565.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
 KW diabetic neuropathy; arthritic pain; migraine headache;  
 KW infantile epilepsy; ataxia; ss.

XX Synthetic.

XX WO2004016754-A2.

XX 26-FEB-2004.

XX 14-AUG-2003; 2003WO-US025465.

PR 14-AUG-2002; 2002US-0403416P.

XX (PHAA ) PHARMACIA CORP.

XX Roberds SL;

XX WPI; 2004-203785/19.

XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT Nav1.3, useful for treating a disease or condition associated  
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 PT disorder, or ataxia.

XX Claim 4; SEQ ID NO 565; 417pp; English.

XX The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 18.4%; Score 14.2; DB 1; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 55;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 34 TCCTCTGAGAGCTAAAGAG 52  
 |||||  
 Db 19 TCCTCTGAGAGCTAAAGAG 1

RESULT 37

ADP12043/c

ID ADP12043 standard; DNA; 20 BP.

XX ADP12043;

```

XX DT 12-AUG-2004 (first entry)
XX DE Set 2 right PCR primer for marker probe #149.
XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
XX KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; SS; primer.
XX OS Homo sapiens.
XX PN WO2004042346-A2.
XX PD 21-MAY-2004.
XX PF 24-APR-2003; 2003WO-US012946.
XX PR 24-APR-2002; 2002US-00131831.
XX PR 20-DEC-2002; 2002US-00325999.
XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX PI Rosenberg S;
XX PF WI; 2004-400724/37.
XX PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX PT rejection, in an individual, comprises detecting the expression level of
XX PT the genes.
XX PS Claim 58; SEQ ID NO 2052; 1762pp; English.
XX CC The present invention relates to diagnosing or monitoring transplant
XX CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX CC comprises detecting the expression level of one or more genes. The
XX CC methods, system and kits are useful in diagnosing or monitoring
XX CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX CC islet, lung, bone marrow or stem cell transplant rejection,
XX CC xenotransplant rejection or mechanical organ replacement rejection, in an
XX CC individual. The method is also useful in assessing the immune status of
XX CC an individual. The methods are also useful in diagnosing and monitoring
XX CC diseases that involve the immune system, e.g. rheumatoid arthritis,
XX CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX CC viral, bacterial or fungal infection. The present sequence represents a
XX CC primer for a 50 mer oligonucleotide marker for diagnosis and monitoring
XX CC of allograft rejection and other disorders.
XX SQ Sequence 20 BP; 2 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
    Query Match 18.4%; Score 14.2; DB 1; Length 20;
    Best Local Similarity 84.2%; Pred. No. 55;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 32 AGTCCTCTGAGAGGTAAG 50
    |||||
DB 20 ACTCTCCGAGGCAAG 2
    |||||

RESULT 38
ABN10033
ID ABN10033 standard; DNA; 17 BP.
XX AC ABN10033;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10025.
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; SS.

OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PA (ABOM-) ABOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX PF WI; 2002-179446/23.
XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX PT or as specific biomolecule capture probes for surface-enhanced laser
XX PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX PS Disclosure; SEQ ID NO 10025; 214pp; English.
XX CC The present invention describes a human genome-derived myosin-like
XX CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX CC nucleic acids can be used as probes to detect, characterise and quantify
XX CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX CC provide initial substrates for the recombinant engineering of hGDMPLP-1
XX CC protein variants having desired phenotypic improvements, and for
XX CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX CC -1 proteins, as standards in assays used to determine the concentration
XX CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX CC capture probes for surface-enhanced laser desorption/ionisation, as
XX CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX CC production, and in vaccines or for replacement therapy. The
XX CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX CC disorder associated with the expression of hGDMPLP-1, in particular heart
XX CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX CC The present sequence represents an oligomer used in the screening of the
XX CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequence
XX SQ Sequence 17 BP; 1 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
    Query Match 18.2%; Score 14; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 49;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 TCTGGAGTCTCTG 40
    |||||
DB 3 TCTGGAGTCTCTG 16

RESULT 39
ABN10032
ID ABN10032 standard; DNA; 17 BP.

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CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
 Query Match 18.2%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 27 TCTGGAGTCTCTCG 40  
 Db 4 TCTGGAGTCTCTCG 17  
 RESULT 41  
 ACN73123  
 ID ACN73123 standard; DNA; 17 BP.  
 XX  
 AC ACN73123;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human GDMLP-1 probe SEQ ID NO:10025.  
 XX  
 KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;  
 KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004137589-A1.  
 XX  
 PD 15-JUL-2004.  
 XX  
 PF 26-NOV-2003; 2003US-00723361.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US0000661.  
 PR 30-JAN-2001; 2001WO-US0000662.  
 PR 30-JAN-2001; 2001WO-US0000663.  
 PR 30-JAN-2001; 2001WO-US0000664.  
 PR 30-JAN-2001; 2001WO-US0000665.  
 PR 30-JAN-2001; 2001WO-US0000666.  
 PR 30-JAN-2001; 2001WO-US0000667.  
 PR 30-JAN-2001; 2001WO-US0000668.  
 PR 30-JAN-2001; 2001WO-US0000669.  
 PR 05-FEB-2001; 2001US-0266860P.  
 PR 25-MAY-2001; 2001US-00866108.  
 XX  
 PA (GUY/) GU Y.  
 PA (JIY/) JI Y.  
 PA (PENN/) PENN S G.  
 PA (HANZ/) HANZEL D K.  
 PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.  
 PA (SHAN/) SHANNON M E.  
 XX  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 XX WPI; 2004-533378/51.  
 XX  
 XX Novel myosin-like protein-1, useful for treating or preventing disorder  
 XX associated with decreased expression or activity of human genome-derived  
 XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 XX function.  
 XX  
 XX Disclosure; SEQ ID NO 10025; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (SI) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (SI), 95% deviation from (SI) which are conservative substitutions, and  
 CC 65% identity to (SI). A polypeptide of the invention acts as an agonist or  
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 1 A; 4 C; 5 G; 7 T; 0 U; 0 Other;  
 Query Match 18.2%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 27 TCTGGAGTCTCTCG 40  
 Db 3 TCTGGAGTCTCTCG 16  
 RESULT 42  
 ADC04443/c  
 ID ADC04443 standard; DNA; 17 BP.  
 XX  
 AC ADC04443;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human Na/H exchanger-like protein 1 gene oligonucleotide #890.  
 XX  
 KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;  
 KW NHEPLP; passive replacement therapy; vaccine; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1273660-A2.  
 XX  
 PD 08-JAN-2003.  
 XX  
 PF 25-JAN-2002; 2002EP-00001160.  
 XX  
 PR 30-JAN-2001; 2001WO-US0000666.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 21-DEC-2001; 2001US-0343331P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Gu Y;  
 XX  
 DR WPI; 2003-302724/30.  
 XX  
 PT New human sodium-hydrogen exchanger like protein 1 (NHEPLP), useful as a  
 PT passive replacement therapy or as a vaccine for treating or preventing  
 PT disorders associated with aberrant expression or activity of human  
 PT NHEPLP.  
 XX  
 PS Example 2; SEQ ID NO 930; 468pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule which encodes a Na<sup>+</sup>/H<sup>+</sup>  
 CC exchanger like protein (NHEPLP). The NHEPLP nucleic acid molecule, NHEPLP  
 CC polypeptide, an antibody against the protein or its antigen-binding  
 CC fragment is useful in therapy. The NHEPLP nucleic acid molecule, NHEPLP  
 CC polypeptide and an agonist are particularly useful for manufacturing a  
 CC medicament for treating or preventing a disorder associated with  
 CC decreased expression or activity of human NHEPLP. The antibody or its  
 CC antigen-binding fragment, and an antagonist, are useful for manufacturing  
 CC a medicament for treating or preventing a disorder associated with  
 CC increased expression or activity of human NHEPLP. The NHEPLP nucleic acid  
 CC or protein is useful as passive replacement therapy, as a vaccine, or in



CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide  
 CC spanning the sequence of the human NHEP1 gene (ADC03514).

XX Sequence 17 BP; 2 A; 5 C; 3 G; 7 T; 0 U; 0 Other;  
 SQ Query Match 17.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 53;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 47 AAAGAGCCGCGAAGCT 63  
 DB 17 AATGAGCCGCGAAGAT 1

RESULT 43  
 ADJ82395  
 ID ADJ82395 standard; DNA; 15 BP.

XX AC ADJ82395;  
 DT 06-MAY-2004 (first entry)  
 XX KLMSY-encoding nucleotide #123.

DE ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;

XX KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;  
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;  
 KW myeloproliferative disease; blood vessel proliferative disease;  
 KW angiogenesis.

XX Synthetic.

XX WO2003045973-A2.

XX 05-JUN-2003.

XX 30-SEP-2002; 2002WO-US031165.

XX 28-NOV-2001; 2001US-0333476P.

XX (BECT) BECTON DICKINSON & CO.  
 PA (HAAL/) HAALAND P D.

XX Dean C, Heidaran M, Spargo CA;

XX WPI; 2003-505179/47.

XX New peptides having growth inhibitory action, useful for inhibiting tumor  
 PT or cancer cell proliferation, or for treating fibrotic disorders,  
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)  
 PT disorders.

XX Disclosure; SEQ ID NO 176; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no  
 CC more than about 50 amino acid residues which when contacted with cells in  
 CC which a platelet-derived growth factor receptor (PDGF-R) is activated in  
 CC an autocrine manner, inhibits the growth of these cells. The isolated  
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-  
 CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-  
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell  
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,  
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,  
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,  
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,  
 CC muscle or bone cell. The peptides are also useful for treating fibrotic  
 CC disorders, myeloproliferative diseases, and blood vessel proliferative  
 CC (angiogenic) disorders. This sequence represents a possible nucleotide  
 CC encoding the P3 peptide.

XX Sequence 15 BP; 4 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

XX Query Match 17.4%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 52;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGCTCTGT 73  
 DB 1 AAGCTGATGCTCTAT 15

RESULT 44

ABN10036  
 ID ABN10036 standard; DNA; 17 BP.

XX AC ABN10036;

XX 29-MAY-2002 (first entry)

XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10028.

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US015981.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 05-FEB-2001; 2001WO-US000670.

XX 05-FEB-2001; 2001US-0266860P.

XX (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX Disclosure; SEQ ID NO 10028; 214pp; English.

XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterize and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a



CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 61;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGGAGTCCTCTGAG 42  
 Db 1 CTGGAGTCCTCTGTG 15

RESULT 45  
 ID ABT38020 standard; DNA; 17 BP.  
 XX AC ABT38020;  
 XX DT 12-JUN-2003 (first entry)  
 XX DE Tumour suppression related human fukutin oligo SEQ ID No 3657.  
 XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; protein chip; gene therapy; tumour suppression;  
 KW human fukutin; ds.  
 XX OS Homo sapiens.  
 XX PN W02003025175-A2.  
 XX PD 27-MAR-2003.  
 XX PF 17-SEP-2002; 2002WO-IB004208.  
 XX PR 17-SEP-2001; 2001FR-00011978.  
 XX PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX PI Telerman A, Amson R, Tuijnder M;  
 XX WPI; 2003-333353/30.  
 XX DR New isolated nucleic acid, useful for treating viral diseases associated  
 XX PT with tumors and cell degeneration, also related polypeptides, antibodies  
 XX PT and transfected cells.  
 XX PS Disclosure; Page 461; 720pp; French.  
 XX

CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
 CC given in the specification, a sequence containing at least 15 consecutive  
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
 CC hybridizes to them under highly stringent conditions, or the complement  
 CC of any of them, or the corresponding RNA. The novel isolated nucleic  
 CC acids of the invention are useful as probes and primers for detecting,  
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
 CC component of a gene chip, in vitro as (anti-) sense reagents, and for  
 CC production of recombinant polypeptides. Any of the nucleic acids,  
 CC polypeptides, vectors containing the nucleic acids, cells containing the  
 CC vector or antibodies directed against the polypeptides are useful for  
 CC preparation of pharmaceuticals for prevention and/or treatment of viral  
 CC diseases that are characterised by development of tumours or cell  
 CC degeneration, specifically cancer but also Alzheimer's disease and  
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
 CC patient samples is useful for diagnosis and/or prognosis of these

CC diseases. The polypeptides can also be used to generate antibodies, and  
 CC both the polypeptide and antibodies are useful as components of protein  
 CC chips. The nucleic acid sequences of the invention can be used in gene  
 CC therapy. This polynucleotide sequence represents a tumour suppression  
 CC related human fukutin oligonucleotide of the invention  
 XX  
 SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 61;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 29 TGGAGTCCTCTGAGA 43  
 Db 17 TGGAGTCCTCTGAGA 3

RESULT 46  
 ID ADC04444 standard; DNA; 17 BP.  
 XX AC ADC04444;  
 XX DT 18-DEC-2003 (first entry)  
 XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #891.  
 XX KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;  
 KW NHEPLP1; passive replacement therapy; vaccine; diagnosis.  
 XX OS Homo sapiens.  
 XX PN EP1273660-A2.  
 XX PD 08-JAN-2003.  
 XX PF 25-JAN-2002; 2002EP-00001160.  
 XX PR 30-JAN-2001; 2001WO-US000666.  
 XX PR 23-MAY-2001; 2001US-00864761.  
 XX PR 21-DEC-2001; 2001US-0343331P.  
 XX PA (AEOM-) AEOMICA INC.  
 XX PI Gu Y;  
 XX WPI; 2003-302724/30.  
 XX DR New human sodium-hydrogen exchanger like protein 1 (NHEPLP1), useful as a  
 XX PT passive replacement therapy or as a vaccine for treating or preventing  
 XX PT disorders associated with aberrant expression or activity of human  
 XX NHEPLP1.  
 XX PS Example 2; SEQ ID NO 931; 468pp; English.  
 XX

CC The invention relates to a nucleic acid molecule which encodes a Na+/H+  
 CC exchanger like protein (NHEPLP1). The NHEPLP1 nucleic acid molecule, NHEPLP1  
 CC polypeptide, an antibody against the protein or its antigen-binding  
 CC fragment is useful in therapy. The NHEPLP1 nucleic acid molecule, NHEPLP1  
 CC polypeptide and an agonist are particularly useful for manufacturing a  
 CC medicament for treating or preventing a disorder associated with  
 CC decreased expression or activity of human NHEPLP1. The antibody or its  
 CC antigen-binding fragment, and an antagonist, are useful for manufacturing  
 CC a medicament for treating or preventing a disorder associated with  
 CC increased expression or activity of human NHEPLP1. The NHEPLP1 nucleic acid  
 CC or protein is useful as passive replacement therapy, as a vaccine, or in  
 CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide  
 CC spanning the sequence of the human NHEPLP1 gene (ADC03514).  
 XX  
 SQ Sequence 17 BP; 1 A; 5 C; 3 G; 8 T; 0 U; 0 Other;  
 Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 61;



XX DE Human tumour suppression/reversion-related DNA sequence SeqID3647.  
 XX XX  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW cytosstatic; viricide; neuroprotective; neurotropic; neuroleptic; probe;  
 KW primer; PCR; gene chip; antisense; viral disease; tumour;  
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX OS Homo sapiens.  
 XX XX WO2003025177-A2.  
 XX XX 27-MAR-2003.  
 XX XX  
 PF 17-SEP-2002; 2002WO-IB004523.  
 XX XX  
 PR 17-SEP-2001; 2001FR-00011980.  
 XX XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX XX  
 DR WPI; 2003-313354/30.  
 XX XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX XX  
 PS Disclosure; SEQ ID NO 3647; 30pp; French.  
 XX XX  
 CC This invention relates to novel isolated nucleic acid sequences involved  
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
 CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytostatic, viricide, neuroprotective,  
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, identifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publishedpct\_sequences  
 XX XX  
 SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 61;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 29 TGGAGTCTCTGAGA 43  
 Db 17 TGGAGTCTCTGAGA 3  
 RESULT 50  
 ACN73126  
 ID ACN73126 standard; DNA; 17 BP.  
 XX AC ACN73126;  
 XX XX  
 DT 02-DEC-2004 (first entry)  
 XX XX  
 DE Human GDMPL-1 probe SEQ ID NO:10028.  
 XX XX  
 KW Human; ss; probe; myosin-like protein-1; hGDMPL-1;  
 KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX XX  
 OS Homo sapiens.  
 XX XX  
 PN US2004137589-A1.  
 XX XX  
 PD 15-JUL-2004.  
 XX XX  
 PF 26-NOV-2003; 2003US-00723361.  
 XX XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 XX XX

XX PN FR2826373-A1.  
 XX XX  
 PD 27-DEC-2002.  
 XX XX  
 PF 20-JUN-2001; 2001FR-00008139.  
 XX XX  
 PR 20-JUN-2001; 2001FR-00008139.  
 XX XX  
 PA (MOLE-) MOLECULAR ENGINES LAB SA.  
 XX XX  
 PI Tuijnder M, Telerman A, Amson R;  
 XX XX  
 DR WPI; 2003-250498/25.  
 XX XX  
 PT New nucleic acid sequences associated with tumour suppression, regression,  
 PT apoptosis or virus resistance are useful to diagnose and treat viral  
 PT disease, development of tumor cells and cell degeneration.  
 XX XX  
 PS Claim 1; Page 612; 798pp; French.  
 XX XX  
 CC This sequence represents an isolated nucleic acid sequence associated  
 CC with tumour suppression or regression, apoptosis or virus resistance. The  
 CC invention relates to these sequences or sequences having at least 80%  
 CC identity to them, and polypeptides encoded by the sequences or  
 CC polypeptides having 80% identity to the polypeptide sequences. The  
 CC invention is used to diagnose or treat viral disease or disease  
 CC characterized by development of tumour cells or cellular degeneration  
 XX XX  
 SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 61;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 29 TGGAGTCTCTGAGA 43  
 Db 17 TGGAGTCTCTGAGA 3  
 RESULT 51  
 ACN73126  
 ID ACN73126 standard; DNA; 17 BP.  
 XX AC ACN73126;  
 XX XX  
 DT 02-DEC-2004 (first entry)  
 XX XX  
 DE Human GDMPL-1 probe SEQ ID NO:10028.  
 XX XX  
 KW Human; ss; probe; myosin-like protein-1; hGDMPL-1;  
 KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX XX  
 OS Homo sapiens.  
 XX XX  
 PN US2004137589-A1.  
 XX XX  
 PD 15-JUL-2004.  
 XX XX  
 PF 26-NOV-2003; 2003US-00723361.  
 XX XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 XX XX

PR 30-JAN-2001; 2001WO-US0006568.  
 PR 30-JAN-2001; 2001WO-US0006669.  
 PR 30-JAN-2001; 2001WO-US0006670.  
 PR 03-FEB-2001; 2001US-0266860P.  
 PR 25-MAY-2001; 2001US-00866108.  
 XX  
 PA (GUYX/) GU Y.  
 PA (JIVV/) JI Y.  
 PA (PENN/) PENN S G.  
 PA (HANKZ/) HANZEL D K.  
 PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.  
 PA (SHAN/) SHANNON M E.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 XX WPI; 2004-533378/51.  
 DR  
 XX Novel myosin-like protein-1, useful for treating or preventing disorder  
 PT associated with decreased expression or activity of human genome-derived  
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 PT function.  
 XX  
 PS Disclosure; SEQ ID NO 10028; 0pp; English.  
 XX  
 CC The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGMDLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
 CC antagonist of hGMDLP-1, or as an inhibitor of hGMDLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGMDLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 17.4%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 61;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 28 CTGAGGTCCTCTGAG 42  
 DB |||||  
 1 CTGAGGTCCTCTG 15  
 XX  
 RESULT 52  
 AAQ55741/C  
 ID AAQ55741 standard; DNA; 18 BP.  
 XX  
 AC AAQ55741;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 22-JUL-1994 (first entry)  
 XX  
 DE LCR Oligo A.  
 XX  
 KW Ligase chain reaction; LCR; Pyrococcus furiosus; ligation; Pfu;  
 KW hyperthermophilic archaeobacterium; catalysis; blunt-end; Tth;  
 KW Thermus thermophilus; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9402615-A1.  
 XX  
 PD 03-FEB-1994.  
 XX  
 PF 22-JUL-1993; 93WO-US0006939.  
 DT 22-JUL-1994 (first entry)  
 XX  
 PR 23-JUL-1992; 92US-00919140.  
 XX  
 PA (STRA-) STRATAGENE.  
 XX  
 PI Mathur EJ, Marsh EJ, Schoettlin WE;  
 KW WPI; 1994-048873/06.  
 XX  
 PT Thermostable DNA ligase from Pyrococcus furiosus - has improved ligation  
 PT specificity and stability at high temperatures, giving greater efficiency  
 PT in ligase chain reaction.  
 XX  
 PS Example 12; Page 56; 84pp; English.  
 XX  
 CC Four oligonucleotide probes (AAQ55741-44) and two oligonucleotide  
 CC templates (AAQ55739-40) were used in a ligase chain reaction of  
 CC recombinant Pfu DNA ligase. The assay shows that both Tth DNA ligase and  
 CC Pfu DNA ligase perform well in LCR after multiple cycles forming a single  
 CC LCR DNA fragment without appreciable blunt-end ligation or background  
 CC reaction prods. However, the Tth DNA ligase in not heat stable when  
 CC exposed to temps. required to separate the strands of double-stranded  
 CC genomic DNA. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 18 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 17.1%; Score 13.2; DB 1; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 69;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 18 GGATACAACTCTGGAGTC 35  
 DB |||||  
 18 GGACACACACTTGGAGTC 1  
 XX  
 RESULT 53  
 AAQ55744  
 ID AAQ55744 standard; DNA; 18 BP.  
 XX  
 AC AAQ55744;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 22-JUL-1994 (first entry)  
 XX  
 DE LCR Oligo D.  
 XX  
 KW Ligase chain reaction; LCR; Pyrococcus furiosus; ligation; Pfu;  
 KW hyperthermophilic archaeobacterium; catalysis; blunt-end; Tth;  
 KW Thermus thermophilus; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9402615-A1.  
 XX  
 PD 03-FEB-1994.  
 XX  
 PF 22-JUL-1993; 93WO-US0006939.  
 DT 22-JUL-1994 (first entry)  
 XX  
 PR 23-JUL-1992; 92US-00919140.  
 XX  
 PA (STRA-) STRATAGENE.  
 XX  
 PI Mathur EJ, Marsh EJ, Schoettlin WE;  
 KW WPI; 1994-048873/06.  
 XX  
 PT Thermostable DNA ligase from Pyrococcus furiosus - has improved ligation  
 PT specificity and stability at high temperatures, giving greater efficiency  
 PT in ligase chain reaction.  
 XX  
 PS Example 12; Page 56; 84pp; English.  
 XX  
 CC Four oligonucleotide probes (AAQ55741-44) and two oligonucleotide  
 CC templates (AAQ55739-40) were used in a ligase chain reaction of  
 CC recombinant Pfu DNA ligase. The assay shows that both Tth DNA ligase and  
 CC Pfu DNA ligase perform well in LCR after multiple cycles forming a single

PA (STRA-) STRATAGENE.  
 XX Mathur EJ, Marsh EJ, Schoettlin WE;  
 XX WPI; 1994-048873/06.  
 DR  
 XX Thermostable DNA ligase from Pyrococcus furiosus - has improved ligation  
 PT specificity and stability at high temperatures, giving greater efficiency  
 PT in ligase chain reaction.  
 XX  
 PS Example 12; Page 56; 84pp; English.  
 XX  
 CC Four oligonucleotide probes (AAQ55741-44) and two oligonucleotide  
 CC templates (AAQ55739-40) were used in a ligase chain reaction of  
 CC recombinant Pfu DNA ligase. The assay shows that both Tth DNA ligase and  
 CC Pfu DNA ligase perform well in LCR after multiple cycles forming a single  
 CC LCR DNA fragment without appreciable blunt-end ligation or background  
 CC reaction prods. However, the Tth DNA ligase in not heat stable when  
 CC exposed to temps. required to separate the strands of double-stranded  
 CC genomic DNA. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 18 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 17.1%; Score 13.2; DB 1; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 69;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 18 GGATACAACTCTGGAGTC 35  
 DB |||||  
 18 GGACACACACTTGGAGTC 1  
 XX  
 RESULT 53  
 AAQ55744  
 ID AAQ55744 standard; DNA; 18 BP.  
 XX  
 AC AAQ55744;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 22-JUL-1994 (first entry)  
 XX  
 DE LCR Oligo D.  
 XX  
 KW Ligase chain reaction; LCR; Pyrococcus furiosus; ligation; Pfu;  
 KW hyperthermophilic archaeobacterium; catalysis; blunt-end; Tth;  
 KW Thermus thermophilus; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9402615-A1.  
 XX  
 PD 03-FEB-1994.  
 XX  
 PF 22-JUL-1993; 93WO-US0006939.  
 DT 22-JUL-1994 (first entry)  
 XX  
 PR 23-JUL-1992; 92US-00919140.  
 XX  
 PA (STRA-) STRATAGENE.  
 XX  
 PI Mathur EJ, Marsh EJ, Schoettlin WE;  
 KW WPI; 1994-048873/06.  
 XX  
 PT Thermostable DNA ligase from Pyrococcus furiosus - has improved ligation  
 PT specificity and stability at high temperatures, giving greater efficiency  
 PT in ligase chain reaction.  
 XX  
 PS Example 12; Page 56; 84pp; English.  
 XX  
 CC Four oligonucleotide probes (AAQ55741-44) and two oligonucleotide  
 CC templates (AAQ55739-40) were used in a ligase chain reaction of  
 CC recombinant Pfu DNA ligase. The assay shows that both Tth DNA ligase and  
 CC Pfu DNA ligase perform well in LCR after multiple cycles forming a single

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CC LCR DNA fragment without appreciable blunt-end ligation or background
CC reaction prods. However, the Tth DNA ligase is not heat stable when
CC exposed to temps. required to separate the strands of double-stranded
CC genomic DNA. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 1 GGACACCACTTGGAGTC 18

RESULT 54
AAT14934/c
ID AAT14934 standard; DNA; 18 BP.
XX
AC AAT14934;
XX
XX 25-MAR-2003 (revised)
DT 26-SEP-1996 (first entry)
XX
XX Oligo A probe for Pfu DNA ligase LCR assay.
DE thermostable ligase; Pfu; Pyrococcus furiosus; ligase chain reaction;
KW LCR; template dependent ligation; ss.
XX
XX Synthetic.
XX
XX US5506137-A.
PN
XX 09-APR-1996.
PD
XX 22-JUL-1993; 93US-00096947.
PF
XX 23-JUL-1992; 92US-00919140.
PR
XX (STRA-) STRATAGENE.
PA
XX Schoettlin WE, Mathur EJ, Marsh EJ;
PI WPI; 1996-200280/20.
XX
XX Plasmid contg. gene for thermostable DNA ligase - useful in ligase chain
XX reactions, stable up to 100 deg. C.
PT
XX Example 12; Col 25-26; 29pp; English.
PS
XX Recombinant Pyrococcus furiosus (Pfu) DNA ligase (AAR96967) activity was
CC assayed in a ligase chain reaction (LCR). The DNA templates consist of
CC two complementary 36-mer synthetic oligonucleotides (AAT14933). The
CC probes consist of 18-mer oligonucleotides (see AAT14934-37). The results
CC illustrated that both Tth and Pfu DNA ligase perform well in LCR after
CC multiple cycles forming a single LCR DNA fragment without appreciable
CC blunt-end ligation or background reaction products. Pfu DNA ligase was
CC able to perform well in LCR without a "pre-melting" step, whereas Tth DNA
CC ligase produced no detectable LCR product indicating that the Tth DNA
CC ligase is not heat stable when exposed to temperatures required to
CC separate the strands of double-stranded genomic DNA. (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX
XX Sequence 18 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACCACTTGGAGTC 1

RESULT 55
AAT14937
ID AAT14937 standard; DNA; 18 BP.
XX
XX AAT14937;
AC
XX 25-MAR-2003 (revised)
DT 26-SEP-1996 (first entry)
XX
XX Oligo D probe for Pfu DNA ligase LCR assay.
DE thermostable ligase; Pfu; Pyrococcus furiosus; ligase chain reaction;
KW LCR; template dependent ligation; ss.
XX
XX Synthetic.
XX
XX US5506137-A.
PN
XX 09-APR-1996.
PD
XX 22-JUL-1993; 93US-00096947.
PF
XX 23-JUL-1992; 92US-00919140.
PR
XX (STRA-) STRATAGENE.
PA
XX Schoettlin WE, Mathur EJ, Marsh EJ;
PI WPI; 1996-200280/20.
XX
XX Plasmid contg. gene for thermostable DNA ligase - useful in ligase chain
XX reactions, stable up to 100 deg. C.
PT
XX Example 12; Col 25-26; 29pp; English.
PS
XX Recombinant Pyrococcus furiosus (Pfu) DNA ligase (AAR96967) activity was
CC assayed in a ligase chain reaction (LCR). The DNA templates consist of
CC two complementary 36-mer synthetic oligonucleotides (AAT14933). The
CC probes consist of 18-mer oligonucleotides (see AAT14934-37). The results
CC illustrated that both Tth and Pfu DNA ligase perform well in LCR after
CC multiple cycles forming a single LCR DNA fragment without appreciable
CC blunt-end ligation or background reaction products. Pfu DNA ligase was
CC able to perform well in LCR without a "pre-melting" step, whereas Tth DNA
CC ligase produced no detectable LCR product indicating that the Tth DNA
CC ligase is not heat stable when exposed to temperatures required to
CC separate the strands of double-stranded genomic DNA. (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACCACTTGGAGTC 1

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RESULT 55
AAT14937
ID AAT14937 standard; DNA; 18 BP.
XX
XX AAT14937;
AC
XX 25-MAR-2003 (revised)
DT 26-SEP-1996 (first entry)
XX
XX Oligo D probe for Pfu DNA ligase LCR assay.
DE thermostable ligase; Pfu; Pyrococcus furiosus; ligase chain reaction;
KW LCR; template dependent ligation; ss.
XX
XX Synthetic.
XX
XX US5506137-A.
PN
XX 09-APR-1996.
PD
XX 22-JUL-1993; 93US-00096947.
PF
XX 23-JUL-1992; 92US-00919140.
PR
XX (STRA-) STRATAGENE.
PA
XX Schoettlin WE, Mathur EJ, Marsh EJ;
PI WPI; 1996-200280/20.
XX
XX Plasmid contg. gene for thermostable DNA ligase - useful in ligase chain
XX reactions, stable up to 100 deg. C.
PT
XX Example 12; Col 25-26; 29pp; English.
PS
XX Recombinant Pyrococcus furiosus (Pfu) DNA ligase (AAR96967) activity was
CC assayed in a ligase chain reaction (LCR). The DNA templates consist of
CC two complementary 36-mer synthetic oligonucleotides (AAT14933). The
CC probes consist of 18-mer oligonucleotides (see AAT14934-37). The results
CC illustrated that both Tth and Pfu DNA ligase perform well in LCR after
CC multiple cycles forming a single LCR DNA fragment without appreciable
CC blunt-end ligation or background reaction products. Pfu DNA ligase was
CC able to perform well in LCR without a "pre-melting" step, whereas Tth DNA
CC ligase produced no detectable LCR product indicating that the Tth DNA
CC ligase is not heat stable when exposed to temperatures required to
CC separate the strands of double-stranded genomic DNA. (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 1 GGACACCACTTGGAGTC 18

RESULT 56
AAT13161/c
ID AAT13161 standard; DNA; 18 BP.
XX
XX AAT13161;
AC
XX 16-OCT-2001 (first entry)
DT
XX Human MTSPl protease domain 5' end cDNA RACE sense PCR primer.
DE
XX Human; transmembrane serine protease; membrane-type serine protease;
KW MTSPl; protease domain; neoplastic disease; tumour; cancer; cytostatic;

```

KW lung carcinoma; colon adenocarcinoma; ovarian carcinoma; gene therapy;  
 KW rapid amplification of cDNA ends; RACE; PCR primer; ss.  
 OS Homo sapiens.  
 XX WO200157194-A2.  
 XX  
 XX 09-AUG-2001.  
 XX  
 XX 02-FEB-2001; 2001WO-US003471.  
 XX  
 XX 03-FEB-2000; 2000US-0179982P.  
 PR 18-FEB-2000; 2000US-0183542P.  
 PR 22-JUN-2000; 2000US-0213124P.  
 PR 26-JUL-2000; 2000US-0220970P.  
 PR 08-SEP-2000; 2000US-00657986.  
 PR 22-SEP-2000; 2000US-0234840P.  
 XX  
 PA (CORV-) CORVAS INT INC.  
 XX  
 XX Madison EL, Ong EO, Yeh J;  
 PI  
 XX WPI; 2001-488877/53.  
 DR  
 XX Novel single chain polypeptide comprising protease domain of type-II  
 PT membrane-type serine protease or its catalytically active portion useful  
 PT for treating and preventing cancer and tumor.  
 XX  
 XX Example 6; Page 164; 256pp; English.  
 XX  
 CC The invention relates to transmembrane serine proteases and their  
 CC corresponding nucleotides and the protease domain of a type-II membrane-  
 CC type serine protease (MTSP). MTSP is useful for identifying compounds  
 CC that modulate or inhibit its proteolytic activity and for formulating a  
 CC medicament for treating neoplastic disease. MTSP and its corresponding  
 CC nucleotides are useful in preventing or treating tumours or cancers such  
 CC as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in  
 CC diagnostics and in hybridisation assays. MTSP is useful as a diagnostic  
 CC marker for tumour development, growth and/or progression and as  
 CC immunogens to generate antibodies that specifically bind to it. MTSP DNA  
 CC is useful in a yeast two-hybrid system and in gene therapy. The present  
 CC sequence is a gene-specific RACE (rapid amplification of cDNA ends) PCR  
 CC primer used to obtain 5' region of cDNA encoding protease domain of MTSP1  
 XX  
 SQ Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 17.1%; Score 13.2; DB 1; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 69;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 30 GGAGTCCTCTGAGAGGTA 47  
 Db 18 GGAGTCGTAGGAGGTA 1  
 RESULT 57  
 AAD36932/C  
 ID AAD36932 standard; DNA; 18 BP.  
 XX  
 AC AAD36932;  
 XX  
 XX 21-AUG-2002 (first entry)  
 DT  
 XX Human MTSP1 protease domain cDNA amplifying sense PCR primer.  
 DE  
 XX Human; amide derivative; serine protease; matrilptase; MTSP1; cancer;  
 KW therapy; tumour; metastasis; cytostatic; PCR; primer; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200220475-A2.  
 PN  
 XX 14-MAR-2002.  
 PD

XX 07-SEP-2001; 2001WO-US028137.  
 XX  
 XX 08-SEP-2000; 2000US-00657986.  
 PR  
 XX (CORV-) CORVAS INT INC.  
 PA  
 XX Duncan DF, Madison EL, Semple JE, Coombs GS, Reiner JE, Ong EO;  
 PI Araldi GL;  
 PI  
 XX WPI; 2002-415722/44.  
 DR  
 XX Amide derivatives, useful as serine protease inhibitors for reducing  
 XX tumor progression and metastasis.  
 PT  
 XX Example 1; Page 43; 82pp; English.  
 PS  
 XX The invention relates to amide derivative compounds which inhibit serine  
 CC protease activity of matrilptase or MTSP1. Matrilptase and MTSP1 are serine  
 CC proteases reported to be expressed in high levels in certain cancer cell  
 CC lines. The compounds of the invention are useful for treating conditions  
 CC ameliorated by inhibition of the serine protease activity of matrilptase  
 CC or MTSP1. The compounds are also useful in the prevention and treatment  
 CC of cancerous conditions and decrease the growth of cancerous tumours and  
 CC retard metastasis. The present sequence is a PCR primer used for  
 CC amplifying human MTSP1 protease domain cDNA  
 XX  
 SQ Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 17.1%; Score 13.2; DB 1; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 69;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 30 GGAGTCCTCTGAGAGGTA 47  
 Db 18 GGAGTCGTAGGAGGTA 1  
 RESULT 58  
 ADA25180/C  
 ID ADA25180 standard; DNA; 18 BP.  
 XX  
 AC ADA25180;  
 XX  
 XX 20-NOV-2003 (first entry)  
 DT  
 XX Human MTSP1 sense PCR primer.  
 DE  
 XX ss; serine protease; matrilptase; MTSP1; cancer; tumour; colon cancer;  
 KW lung cancer; stomach cancer; rectal cancer; skin cancer; human;  
 KW protease domain; PCR; primer.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US2003050251-A1.  
 PN  
 XX 13-MAR-2003.  
 PD  
 XX 05-MAR-2002; 2002US-00092004.  
 PF  
 XX 08-SEP-2000; 2000US-00657986.  
 PR  
 XX 07-SEP-2001; 2001WO-US028137.  
 PR  
 XX (SEMP/) SEMPLE J E.  
 PA (COOM/) COOMBS G S.  
 PA (REIN/) REINER J E.  
 PA (ONGE/) ONG E O.  
 PA (ARAL/) ARALDI G L.  
 XX  
 XX Semple JE, Coombs GS, Reiner JE, Ong EO, Araldi GL;  
 PI WPI; 2003-625421/59.  
 XX  
 XX

PT Treatment of condition ameliorated by inhibition of serine protease  
 PT activity of matrilysin, e.g. cancerous tumors, retard metastasis or  
 PT cancer of lung, colon and stomach, comprises administration of a peptide  
 PT containing compound.

XX Example 1; Page 14; 34pp; English.

PS The invention relates to a method of treating a condition ameliorated by  
 CC an inhibition or decrease in serine protease activity of matrilysin or  
 CC MTSP1 which comprises administration of a peptide containing compound.  
 CC The compound is useful for treating pathological conditions ameliorated  
 CC by decreasing or inhibiting serine protease activity of matrilysin or  
 CC MTSP1, for the treatment of cancerous conditions, e.g. cancerous tumors,  
 CC colon cancer, lung cancer, stomach cancer, rectal cancer or skin cancer.  
 CC The present sequence represents the human MTSP1 sense PCR primer.

XX Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 17.1%; Score 13.2; DB 1; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 69;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 30 GGAGTCTCTCGAGGTA 47  
 Db 18 GGACTCTAGGAGGTA 1

RESULT 59

ADM57469/C

ID ADM57469 standard; DNA; 18 BP.

XX ADM57469;

XX 03-JUN-2004 (first entry)

XX M. tuberculosis PCR primer RD3-int-REP.R.

XX antibacterial; vaccine; mmpL6; Mycobacterium; BCG; Tbd1; ss; PCR; primer.

XX Mycobacterium tuberculosis.

XX BPI338657-A1.

XX 27-AUG-2003.

XX 25-FEB-2002; 2002EP-00290458.

XX 25-FEB-2002; 2002EP-00290458.

XX (INSP ) INST PASTEUR.

XX Cole S, Brosch R, Gordon S, Eiglmeier K, Garnier T;

XX WPI; 2003-699254/67.

XX New Tbd1 nucleic acids having the mutation CTG to CGG at codon 463 of  
 PT gene katG, useful for distinguishing Mycobacterium tuberculosis infection  
 PT from M. africanum, M. canettii, M. microti, M. bovis, or M. bovis BCG  
 PT infection.

PS Disclosure; Page 19; 73pp; English.

XX The invention relates to a novel isolated or purified nucleic acid. A  
 CC polypeptide encoded by a nucleic acid of the invention has antibacterial  
 CC activity, and may have a use in a vaccine. The nucleic acid is a Tbd1  
 CC nucleic acid having a fully defined sequence of 3953 bp given in the  
 CC specification. The Tbd1 deletion or mmpL6 551 polymorphism is useful as a  
 CC genetic marker for the differentiation of Mycobacterium strain of M.  
 CC tuberculosis complex. The genetic marker in association with at least one  
 CC genetic markers selected from RD1, RD2, RD3, RD4, RD5, RD6, RD7, RD8,  
 CC RD9, RD10, RD11, RD13, RD14, RvD1, RvD2, RvD3, RvD4, RvD5, katG463,  
 CC gyrA95, oxyR285, and pncA57, may be used for the differentiation of  
 CC Mycobacterium strain of M. tuberculosis complex. The nucleic acids may

CC also be used to distinguish an infection resulting from M. tuberculosis  
 CC from an infection resulting from M. africanum, M. canettii, M. microti, M.  
 CC bovis, M. bovis BCG. The present sequence is used in the exemplification  
 CC of the invention.

SQ Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 17.1%; Score 13.2; DB 1; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 69;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AAGAGCGCCTGGGATAC 23  
 Db 18 AAGATCGCCTGGGGATAC 1

RESULT 60

ADJ82396

ID ADJ82396 standard; DNA; 15 BP.

XX ADJ82396;

XX 06-MAY-2004 (first entry)

XX KLM5Y-encoding nucleotide #124.

XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;  
 KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;  
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;  
 KW myeloproliferative disease; blood vessel proliferative disease;  
 KW angiogenesis.

XX Synthetic.

XX WO2003045973-A2.

XX 05-JUN-2003.

XX 30-SEP-2002; 2002WO-US031165.

XX 28-NOV-2001; 2001US-0333476P.

XX (BECT ) BECTON DICKINSON & CO.

XX (HAAL/) HAALAND P D.

XX Dean C, Heidaran M, Spargo CA;

XX WPI; 2003-505179/47.

XX New peptides having growth inhibitory action, useful for inhibiting tumor  
 PT or cancer cell proliferation, or for treating fibrotic disorders,  
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)  
 PT disorders.

PS Disclosure; SEQ ID NO 177; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no  
 CC more than about 50 amino acid residues which when contacted with cells in  
 CC which a platelet-derived growth factor receptor (PDGF-R) is activated in  
 CC an autocrine manner, inhibits the growth of these cells. The isolated  
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-  
 CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-  
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell  
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,  
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,  
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,  
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,  
 CC muscle or bone cell. The peptides are also useful for treating fibrotic  
 CC disorders, myeloproliferative diseases, and blood vessel proliferative  
 CC (angiogenic) disorders. This sequence represents a possible nucleotide  
 CC encoding the P3 peptide.

SQ Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 16.9%; Score 13; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCT 71  
 Db 1 AAGCTGATGTCCT 13

RESULT 61  
 ABN10031  
 ID ABN10031 standard; DNA; 17 BP.  
 AC ABN10031;  
 XX  
 XX 29-MAY-2002 (first entry)  
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10023.  
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200192524-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 PF  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX  
 PS Disclosure; SEQ ID NO 10023; 214pp; English.  
 XX  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 16.9%; Score 13; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCT 39  
 Db 5 TCTGGAGTCTCT 17

RESULT 62  
 ACN73121  
 ID ACN73121 standard; DNA; 17 BP.  
 XX  
 AC ACN73121;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human GDMPLP-1 probe SEQ ID NO:10023.  
 XX  
 KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004137589-A1.  
 XX  
 PD 15-JUL-2004.  
 XX  
 XX 26-NOV-2003; 2003US-00723361.  
 PF  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 PR 25-MAY-2001; 2001US-00866108.  
 XX  
 XX (GUY/) GU Y.  
 PA (JIY/) JI Y.  
 PA (PENN/) PENN S G.  
 PA (HANZ/) HANZEL D K.  
 PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.  
 PA (SHAN/) SHANNON M E.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 XX WPI; 2004-533378/51.  
 DR  
 XX Novel myosin-like protein-1, useful for treating or preventing disorder  
 PT



PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
function.  
PS Disclosure; SEQ ID NO 10023; Opp; English.  
XX  
XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103  
XX  
XX Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 16.9%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 TCTGGAGTCTCTCT 39  
DB 5 TCTGGAGTCTCTCT 17  
RESULT 63  
AAK35522/c  
ID AAK35522 standard; cDNA; 18 BP.  
XX  
XX AAK35522;  
AC  
DT 08-JUL-1999 (first entry)  
XX  
XX PCR primer used to amplify 36B4 gene (in control reactions).  
DE  
XX Facilitative glucose transporter protein; GLUT8; malignancy;  
KW breast cancer; prostate cancer; epithelial cell cancer;  
KW non-insulin-dependent diabetes mellitus; insulin resistance;  
KW central obesity; hypertension; dyslipidaemia; glucose intolerance;  
KW cancer; 36B4 gene; PCR primer; ss.  
XX  
XX Synthetic.  
XX  
XX WO9918125-A1.  
XX  
XX 15-APR-1999.  
XX  
XX 30-SEP-1998; 98WO-AU000819.  
XX  
XX 01-OCT-1997; 97AU-00009573.  
XX  
XX (SVIN-) ST VINCENTS INST MEDICAL RES.  
PA  
XX Rogers SD, Best JD;  
PI  
XX WPI; 1999-277253/23.  
XX  
XX Nucleic acid encoding a facilitative glucose transporter.  
PT  
XX Example 7; Page 17; 72pp; English.  
XX  
XX The specification describes a facilitative glucose transporter protein,  
CC GLUT8, and its functional fragments. Agents that inhibit activity or  
CC expression of GLUT8 (particularly non-utilizable glucose analogues,  
CC antisense sequences or dominant negative mutants) are used to treat  
CC malignancy, particularly cancer of breast, prostate and epithelial cells  
CC (e.g. skin or colon). Agents that upregulate expression of GLUT8 (e.g.  
CC the GLUT8 gene, administered by tissue-localized gene therapy) are used  
CC to treat non-insulin-dependent diabetes mellitus and/or insulin

CC resistance (e.g. central obesity, hypertension, dyslipidaemia or glucose  
CC intolerance). Detecting expression of GLUT8 is used for diagnosis,  
CC monitoring and staging of cancers, particularly of the breast. Antibodies  
CC raised against GLUT8 are useful as immunoassay reagents and as  
CC therapeutic inhibitors. PCR primers AAK35521-22 were used in the course  
CC of the invention  
XX  
XX Sequence 18 BP; 1 A; 8 C; 5 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 16.9%; Score 13; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 50 GAGCCAGCGGAGC 62  
DB 14 GAGCCAGCGGAGC 2  
RESULT 64  
ADC04442/c  
ID ADC04442 standard; DNA; 17 BP.  
XX  
XX ADC04442;  
AC  
XX 18-DEC-2003 (first entry)  
DT  
XX Human Na/H exchanger-like protein 1 gene oligonucleotide #889.  
DE  
XX ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;  
KW NHEPL1; passive replacement therapy; vaccine; diagnosis.  
KW  
XX Homo sapiens.  
OS  
XX EP1273660-A2.  
PN  
XX 08-JAN-2003.  
PD  
XX 25-JAN-2002; 2002BP-00001160.  
PF  
XX 30-JAN-2001; 2001WO-US000666.  
PR  
XX 23-MAY-2001; 2001US-00864761.  
PR  
XX 21-DEC-2001; 2001US-0343331P.  
XX  
XX (AEOM-) AEOMICA INC.  
PA  
XX Gu Y;  
XX  
XX WPI; 2003-302724/30.  
DR  
XX New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a  
PT passive replacement therapy or as a vaccine for treating or preventing  
PT disorders associated with aberrant expression or activity of human  
PT NHEPL1.  
XX  
XX Example 2; SEQ ID NO 929; 468pp; English.  
PS  
XX The invention relates to a nucleic acid molecule which encodes a Na+/H+  
CC exchanger like protein (NHEPL1). The NHEPL1 nucleic acid molecule, NHEPL1  
CC polypeptide, an antibody against the protein or its antigen-binding  
CC fragment is useful in therapy. The NHEPL1 nucleic acid molecule, NHEPL1  
CC polypeptide and an agonist are particularly useful for manufacturing a  
CC medicament for treating or preventing a disorder associated with  
CC decreased expression or activity of human NHEPL1. The antibody or its  
CC antigen-binding fragment, and an antagonist, are useful for manufacturing  
CC a medicament for treating or preventing a disorder associated with  
CC increased expression or activity of human NHEPL1. The NHEPL1 nucleic acid  
CC or protein is useful as passive replacement therapy, as a vaccine, or in  
CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide  
CC spanning the sequence of the human NHEPL1 gene (ADC03514).  
XX  
XX Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 16.6%; Score 12.8; DB 1; Length 17;

```
Best Local Similarity 87.5%; Pred. No. 75;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 AAGAGCCAGCGAGCT 63
DB 17 ATGAGCCAGCGAGAT 2
|||||
17 AAGGCTGCTGGGAT 2

RESULT 66
AAC68677/c
ID AAC68677 standard; DNA; 18 BP.
XX
AC AAC68677;
XX
DT 22-FEB-2001 (first entry)
XX
DE
XX
Chick R35 RNA fingerprinting primer P3.
XX
Chick; R35; uropathic; antiinflammatory; analgesic; gene therapy;
XX seven transmembrane receptor; neuropathic pain; inflammation;
XX incontinence; irritable bowel syndrome; RNA fingerprinting; PCR primer;
XX ss.
XX Gallus gallus.
XX OS
XX WO200064928-A2.
XX PN
XX 02-NOV-2000.
XX PD
XX 20-APR-2000; 2000WO-GB001546.
XX PF
XX 21-APR-1999; 99GB-00009161.
XX PR
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX PA (PLAC ) MAX-PLANCK INST NEUROBIOLOGY.
XX
XX Barde Y, Friedel R, Michalovich D, Reith AD, Schnuerch H;
XX Stubbusch J;
XX WPI; 2000-679669/66.
XX DR
XX Novel R35 polypeptides and polynucleotides useful for treating
XX neuropathic, inflammatory and chronic pain, incontinence and irritable
XX bowel syndrome.
XX
XX Example 1; Page 23; 55pp; English.
XX
XX The present sequence was used to isolate a cDNA fragment of the chick
XX seven transmembrane receptor R35 by RNA fingerprinting. R35 is useful for
XX treating neuropathic pain, inflammatory and chronic pain, incontinence,
XX and disorders of the gastrointestinal tract associated with gut motility
XX and secretion such as irritable bowel syndrome. It is also useful for
XX inducing an immune response in a mammal to protect against the diseases.
XX It is useful in screening assays to identify compounds which stimulate or
XX inhibit the function of the polypeptide, to identify membrane bound or
XX soluble receptors and also for the structure-based design of an agonist,
XX antagonist or inhibitor of R35
XX
XX Sequence 18 BP; 2 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
SQ Query Match 16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 79;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AACAGACGCGCTGGG 18
|||||
DB 16 AACACGACGACCTGGG 1
|||||

RESULT 67
ADG14616
ID ADG14616 standard; DNA; 18 BP.
XX
AC ADG14616;
XX
DT 26-FEB-2004 (first entry)
XX
XX
```

```
Best Local Similarity 87.5%; Pred. No. 75;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 AAGAGCCAGCGAGCT 63
DB 17 ATGAGCCAGCGAGAT 2
|||||
17 AAGGCTGCTGGGAT 2

RESULT 65
ADB45336/c
ID ADB45336 standard; DNA; 17 BP.
XX
AC ADB45336;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #5659.
XX
cytostatic; antiviral; neuroprotective; neuroleptic; ss;
XX primer; probe; tumour suppression; tumour reversion; apoptosis;
XX virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX diagnosis.
XX
XX Homo sapiens.
XX OS
XX WO2003040369-A2.
XX PN
XX 15-MAY-2003.
XX PD
XX 17-SEP-2002; 2002WO-IB004219.
XX PF
XX 17-SEP-2001; 2001PR-00011981.
XX PR
XX (MOLE-) MOLECULAR ENGINES LAB.
XX FA
XX
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX DR
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX
XX Disclosure; Page 693; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules,
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.
XX
XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
SQ Query Match 16.6%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 75;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AAGAGCGCTGGGAT 21
```

DE Human CTLA-4 exon 1 reverse PCR primer, SEQ ID NO:7.  
 KW Therapeutic response; therapeutic outcome; interferon-alpha-2b;  
 KW ribavirin; hepatitis C virus; HCV infection; interleukin-10;  
 KW IL-10 regulatory region; single nucleotide polymorphism; SNP; haplotype;  
 KW genotype; cytotoxic T-lymphocyte antigen-4; CTLA-4 promoter;  
 KW CTLA-4 exon 1; bacterial infection; meningococcal infection;  
 KW rheumatoid arthritis; systemic lupus erythematosus; Sjogren's syndrome;  
 KW inflammatory bowel disease; multiple sclerosis; human; PCR; primer; ss.  
 XX Homo sapiens.  
 XX WO200268699-A1.  
 XX 06-SEP-2002.  
 XX 27-FEB-2002; 2002WO-US006207.  
 XX 27-FEB-2001; 2001US-0271811P.  
 XX (UABR-) UAB RES FOUND.  
 XX Yee L, Tang J, Kaslow RA, Van Leeuwen DJ;  
 XX WPI; 2002-707021/76.  
 XX Predicting a therapeutic response comprises comparing a first nucleic  
 PT acid allele in an interleukin-10 (IL-10) regulatory region with a second  
 PT nucleic acid allele in the IL-10 regulatory region associated with a  
 PT known outcome.  
 XX Claim 41; SEQ ID NO 7; 34pp; English.  
 XX The invention relates to a method for predicting an individual's  
 CC therapeutic response to the administration of interferon-alpha-2b and  
 CC ribavirin for the treatment of a pathological condition, especially  
 CC hepatitis C virus (HCV) infection. The method involves determining which  
 CC allelic form is present at positions -3575, -2763, -1082, -819 and -592  
 CC of the interleukin-10 (IL-10) regulatory region, and comparing these with  
 CC the allelic forms at these positions which are associated with a known  
 CC outcome of interferon-alpha-2b and ribavirin administration. Presence of  
 CC the single nucleotide polymorphisms -592A and -819T, the -592A/A or -  
 CC 819T/T genotypes, the combination of -592A/-819T as a haplotype,  
 CC homozygosity for -592A/-819T, -592A/-819T as a genotype, or possession of  
 CC the (108)TCATA haplotype (encompassing positions -3575, -2763, -1082, -  
 CC 819 and -592) is associated with a sustained response to interferon-alpha  
 CC -2b and ribavirin therapy. In contrast, the presence of -592C and -819C,  
 CC or the (108)TCAC haplotype indicates that the patient will be non-  
 CC responsive to this therapy. The method optionally further comprises  
 CC detection of the allele at position -318 of the cytotoxic T-lymphocyte  
 CC antigen-4 (CTLA-4) promoter and the allele at position 49 of exon 1 of  
 CC the CTLA-4 gene. The invention also encompasses kits and oligonucleotide  
 CC primers for use in the methods of the invention. The method and primers  
 CC are useful for identifying and analyzing genetic polymorphisms in the IL-  
 CC 10 regulatory region and/or cytotoxic T-lymphocyte antigen-4 which can be  
 CC used in predicting an individual's response to therapeutic intervention  
 CC with interferon-alpha-2b and ribavirin for HCV infection, and for  
 CC predicting the responsiveness of an individual to therapy for a  
 CC pathological condition, or for predicting the outcome of therapeutic  
 CC intervention in pathological conditions such as bacterial infection (e.g.  
 CC meningococcal infection), rheumatoid arthritis, systemic lupus  
 CC erythematosus, Sjogren's syndrome, inflammatory bowel disease or multiple  
 CC sclerosis. The present sequence is related to the invention.  
 XX Sequence 18 BP; 7 A; 7 C; 4 G; 0 T; 0 U; 0 Other;  
 XX Query Match 16.6%; Score 12.8; DB 1; Length 18;  
 XX Best Local Similarity 87.5%; Pred. No. 79;  
 XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 47 AAAGAGCGGCGGAGC 62  
 DB 1 ACAGAGCGGCGGAGC 16  
 |||||

## RESULT 68

ADL25789

ID ADL25789 standard; DNA; 18 BP.

XX AC ADL25789;

XX DT 20-MAY-2004 (first entry)

XX DE Human cancer suppressing protein associated PCR primer.

XX KW ss; PCR; human; cancer suppression; cancer; primer.

XX OS Homo sapiens.

XX PN CN1403478-A.

XX PD 19-MAR-2003.

XX PF 12-SEP-2001; 2001CN-00126726.

XX PR 12-SEP-2001; 2001CN-00126726.

XX PA (SHAN-) SHANGHAI XINSHIJI GENE TECH DEV CO LTD.

XX PI Gu J, Yang S;

XX DR WPI; 2003-494227/47.

XX PT Human protein with function of suppressing cancer cell growth and its  
 PT coding sequence.  
 XX Disclosure; Page 12; 43pp; Chinese.

XX The invention relates to one kind of human protein with cancer  
 CC suppressing function, polynucleotides encoding the polypeptide and the  
 CC recombinant process of producing the polypeptide. The present invention  
 CC also discloses the method of using the polypeptide in treating various  
 CC diseases, such as cancer. The present invention also discloses the  
 CC agonist resisting the polypeptide and its treatment effect. The present  
 CC invention also discloses the application of the polynucleotides encoding  
 CC the human protein with cancer suppressing function. The present sequence  
 CC represents a human cancer suppressing protein associated PCR primer.

XX SQ Sequence 18 BP; 6 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

XX Query Match 16.6%; Score 12.8; DB 1; Length 18;

XX Best Local Similarity 87.5%; Pred. No. 79;

XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AAAGAGCGGCGGCGGAT 21

DB 3 AAAGAGCGGCGGCGGAT 18

|||||

## RESULT 69

ADR74794

ID ADR74794 standard; DNA; 18 BP.

XX AC ADR74794;

XX DT 16-DEC-2004 (first entry)

XX DE Allele specific primer B for human stenosis marker hCV25612829.

XX KW Human; ss; PCR; primer; Allele specific primer; coronary stenosis;  
 KW angina; ischaemic chest pain; myocardial infarction;  
 KW sudden cardiac death; SNP; single nucleotide polymorphism.

XX OS Homo sapiens.

XX PN WO2004081186-A2.





PS Disclosure; SEQ ID NO 10029; 214pp; English.

XX The present invention describes a human genome-derived myosin-like

CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1

CC can be used in gene therapy and vaccine production. The hGDMLP-1

CC nucleic acids can be used as probes to detect, characterise and quantify

CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMLP-1

CC protein variants having desired phenotypic improvements, and for

CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be

CC used as immunogens to raise antibodies that specifically recognise hGDMLP

CC -1 proteins, as standards in assays used to determine the concentration

CC and/or amount specifically of hGDMLP proteins, as specific biomolecule

CC capture probes for surface-enhanced laser desorption/ionisation, as

CC therapeutic supplement in patients having specific deficiency in hGDMLP-1

CC production, and in vaccines or for replacement therapy. The

CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a

CC disorder associated with the expression of hGDMLP-1, in particular heart

CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the

CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at [ftp.wipo.int/pub/published\\_pct\\_sequence](http://ftp.wipo.int/pub/published_pct_sequence)

XX

SQ Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 16.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 86;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCTCTGAG 42

DB 1 TGGAGTCTCTG 14

RESULT 73

ABZ65329

ID ABZ65329 standard; RNA; 17 BP.

XX

AC ABZ65329;

XX

DT 21-MAR-2003 (first entry)

XX

DE Human HER2 DNAzyme substrate #786.

XX

KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;

KW anti-rheumatic; cancer; AIDS; ss.

XX

OS Homo sapiens.

XX

PN WO200297114-A2.

XX

PD 05-DEC-2002.

XX

PF 29-MAY-2002; 2002WO-US016840.

XX

PR 29-MAY-2001; 2001US-0294140P.

PR 05-JUN-2001; 2001US-0296249P.

PR 10-SEP-2001; 2001US-0318471P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

XX

PI Mcswiggen J;

XX

XX WPI; 2003-140484/13.

XX

PT Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding

PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX

PS Claim 4; Page 148; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic

CC acid molecule or an enzymatic nucleic acid molecule, that modulates

CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,

CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic

CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-

CC rheumatic activity. The nucleic acid molecules are useful for reducing

CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are

CC also useful for treating breast, ovarian, colorectal, lung, prostate,

CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences

CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,

CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human

CC ribozymes of the invention

XX

SQ Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 16.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 71.4%; Pred. No. 86;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 28 CTGGAGTCTCTGCA 41

DB 4 CUGAGCCCUUGA 17

RESULT 74

ADC04446/C

ID ADC04446 standard; DNA; 17 BP.

XX

AC ADC04446;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human Na/H exchanger-like protein 1 gene oligonucleotide #893.

XX

ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;

KW NHEP1; passive replacement therapy; vaccine; diagnosis.

XX

OS Homo sapiens.

XX

PN BP1273660-A2.

XX

PD 08-JAN-2003.

XX

PF 25-JAN-2002; 2002EP-00001160.

XX

PR 30-JAN-2001; 2001WO-US000666.

PR 23-MAY-2001; 2001US-00864761.

PR 21-DEC-2001; 2001US-0343331P.

XX

PA (AEOM-) AEOMICA INC.

XX

PI Gu Y;

XX

DR WPI; 2003-302724/30.

XX

PT New human sodium-hydrogen exchanger like protein 1 (NHEP1), useful as a

PT passive replacement therapy or as a vaccine for treating or preventing

PT disorders associated with aberrant expression or activity of human

PT NHEP1.

XX

PS Example 2; SEQ ID NO 933; 468pp; English.

XX

CC The invention relates to a nucleic acid molecule which encodes a Na+/H+

CC exchanger like protein (NHEP1). The NHEP1 nucleic acid molecule, NHEP1

CC polypeptide, an antibody against the protein or its antigen-binding

CC fragment is useful in therapy. The NHEP1 nucleic acid molecule, NHEP1

CC polypeptide and an agonist are particularly useful for manufacturing a

CC medicament for treating or preventing a disorder associated with

CC decreased expression or activity of human NHEP1. The antibody or its

CC antigen-binding fragment, and an antagonist, are useful for manufacturing

CC a medicament for treating or preventing a disorder associated with

CC increased expression or activity of human NHEP1. The NHEP1 nucleic acid

CC or protein is useful as passive replacement therapy, as a vaccine, or in  
 CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide  
 CC spanning the sequence of the human NHEP1 gene (ADC03514).  
 XX  
 SQ Sequence 17 BP; 1 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 86;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAGAGCCAGCGAA 60  
 |||||  
 Db 14 AATGAGCCAGCGAA 1

## RESULT 75

ADC04441/c  
 ID ADC04441 standard; DNA; 17 BP.

XX AC ADC04441;

XX DT 18-DEC-2003 (first entry)

XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #888.

XX ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;  
 KW NHEP1; passive replacement therapy; vaccine; diagnosis.  
 XX

XX OS Homo sapiens.

XX PN EP1273660-A2.

XX PD 08-JAN-2003.

XX PF 25-JAN-2002; 2002EP-00001160.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 21-DEC-2001; 2001US-0343331P.

XX PA (ABOM-) ABOMICA INC.

XX PI Gu Y;

XX DR WPI; 2003-302724/30.

XX PT New human sodium-hydrogen exchanger like protein 1 (NHEP1), useful as a  
 PT passive replacement therapy or as a vaccine for treating or preventing  
 PT disorders associated with aberrant expression or activity of human  
 PT NHEP1.

XX PS Example 2; SEQ ID NO 928; 468pp; English.

XX CC The invention relates to a nucleic acid molecule which encodes a Na+/H+  
 CC exchanger like protein (NHEP1). The NHEP1 nucleic acid molecule, NHEP1  
 CC polypeptide, an antibody against the protein or its antigen-binding  
 CC fragment is useful in therapy. The NHEP1 nucleic acid molecule, NHEP1  
 CC polypeptide and an agonist are particularly useful for manufacturing a  
 CC medicament for treating or preventing a disorder associated with  
 CC decreased expression or activity of human NHEP1. The antibody or its  
 CC antigen-binding fragment, and an antagonist, are useful for manufacturing  
 CC a medicament for treating or preventing a disorder associated with  
 CC increased expression or activity of human NHEP1. The NHEP1 nucleic acid  
 CC or protein is useful as passive replacement therapy, as a vaccine, or in  
 CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide  
 CC spanning the sequence of the human NHEP1 gene (ADC03514).  
 XX

SQ Sequence 17 BP; 3 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 16.1%; Score 12.4; DB 1; Length 17;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAAGCT 63  
 |||||  
 Db 16 GAGCCAGCGAAGAT 3

## RESULT 76

ADC04440/c  
 ID ADC04440 standard; DNA; 17 BP.

XX AC ADC04440;

XX DT 18-DEC-2003 (first entry)

XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #887.

XX ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;  
 KW NHEP1; passive replacement therapy; vaccine; diagnosis.  
 XX

XX OS Homo sapiens.

XX PN EP1273660-A2.

XX PD 08-JAN-2003.

XX PF 25-JAN-2002; 2002EP-00001160.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 21-DEC-2001; 2001US-0343331P.

XX PA (ABOM-) ABOMICA INC.

XX PI Gu Y;

XX DR WPI; 2003-302724/30.

XX PT New human sodium-hydrogen exchanger like protein 1 (NHEP1), useful as a  
 PT passive replacement therapy or as a vaccine for treating or preventing  
 PT disorders associated with aberrant expression or activity of human  
 PT NHEP1.

XX PS Example 2; SEQ ID NO 927; 468pp; English.

XX CC The invention relates to a nucleic acid molecule which encodes a Na+/H+  
 CC exchanger like protein (NHEP1). The NHEP1 nucleic acid molecule, NHEP1  
 CC polypeptide, an antibody against the protein or its antigen-binding  
 CC fragment is useful in therapy. The NHEP1 nucleic acid molecule, NHEP1  
 CC polypeptide and an agonist are particularly useful for manufacturing a  
 CC medicament for treating or preventing a disorder associated with  
 CC decreased expression or activity of human NHEP1. The antibody or its  
 CC antigen-binding fragment, and an antagonist, are useful for manufacturing  
 CC a medicament for treating or preventing a disorder associated with  
 CC increased expression or activity of human NHEP1. The NHEP1 nucleic acid  
 CC or protein is useful as passive replacement therapy, as a vaccine, or in  
 CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide  
 CC spanning the sequence of the human NHEP1 gene (ADC03514).  
 XX

SQ Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 16.1%; Score 12.4; DB 1; Length 17;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAAGCT 63  
 |||||  
 Db 17 GAGCCAGCGAAGAT 4

## RESULT 77

ADI47813  
 ID ADI47813 standard; DNA; 17 BP.

XX AC ADI47813;



XX 15-APR-2004 (first entry)  
 XX Human tumour suppression/reversion-related DNA sequence SeqID316.  
 DE  
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;  
 KW primer; PCR; gene chip; antisense; viral disease; tumour;  
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003025177-A2.  
 XX  
 XX 27-MAR-2003.  
 XX  
 XX 17-SEP-2002; 2002WO-IB004523.  
 XX  
 XX 17-SEP-2001; 2001FR-00011980.  
 XX  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 XX Teleman A, Anson R, Tuijnder M;  
 PI  
 XX WPI; 2003-313354/30.  
 XX  
 XX New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 XX Disclosure; SEQ ID NO 316; 30pp; French.  
 XX  
 XX This invention relates to novel isolated nucleic acid sequences involved  
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
 CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytostatic, virucide, neuroprotective,  
 CC nootropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, identifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publishedpct\_sequences  
 XX  
 XX Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 86;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 27 TCTGGAGTCTCTG 40  
 Db ||||| |||||  
 3 TCTGGTGTCTCTG 16  
 RESULT 78  
 AEB58478  
 ID AEB58478 standard; mRNA; 17 BP.  
 XX  
 AC AEB58478;  
 XX  
 XX 22-SEP-2005 (first entry)  
 DT  
 XX Human VEGF receptor 1 (flt-1) DNAzyme target sequence SEQ ID 1056.  
 DE  
 XX VEGF receptor; angiogenesis; cancer; tumor; ocular disease;  
 KW diabetic retinopathy; age related macular degeneration;  
 KW angiogenesis disorder; rheumatoid arthritis; psoriasis; wound healing;

KW endometriosis; endometroid carcinoma; gynecological bleeding disorder;  
 KW mensturation disorder; premenstrual syndrome; menopause; Gynecological;  
 KW Cytostatic; Ophthalmological; Antidiabetic; Antiangiogenic;  
 KW Antipsoriatic; Antirheumatic; Antiarthritic; Vulnerary; Hemostatic;  
 KW Contraceptive; ss; enzymatic nucleic acid.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200296927-A2.  
 XX  
 XX 05-DEC-2002.  
 XX  
 XX 29-MAY-2002; 2002WO-US017674.  
 XX  
 XX 29-MAY-2001; 2001US-00870161.  
 XX  
 XX 30-NOV-2001; 2001US-0334461P.  
 XX  
 XX 03-MAY-2002; 2002US-00138674.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX (CHIR ) CHIRON CORP.  
 PA  
 XX Escobedo J, Mcswiggen J, Pavco P, Stinchcomb D, Sandberg J;  
 PI Gordon G;  
 PI  
 XX WPI; 2003-140439/13.  
 XX  
 XX Novel enzymatic nucleic acids, ribozymes, which modulate expression of  
 PT genes encoding vascular endothelial growth factor and/or VEGF receptor,  
 PT useful for inhibiting tumor angiogenesis in cell, and for treating  
 PT cancer.  
 XX  
 XX Disclosure; SEQ ID NO 1056; 172pp; English.  
 XX  
 XX The invention relates to enzymatic nucleic acids (I) i.e.  
 CC ribozymes/DNAzymes/Zinzymes that target and modulate expression of, genes  
 CC encoding vascular endothelial growth factor (VEGF) and/or VEGF receptor  
 CC (VEGFR1 and 2 encode by the Flt-1 and Kdr genes respectively). Also  
 CC included are a composition comprising (I) and a carrier, administering  
 CC (I) to a cell (by contacting the cell with the compound under conditions  
 CC suitable for the administration), administering (I) to a cell (in  
 CC conjunction with one or more other drug by contacting the cell with the  
 CC compound and the other drug under conditions suitable for the  
 CC administration), administering (I) to a mammal (by contacting the mammal  
 CC with the compound under conditions suitable for the administration),  
 CC treating (M1) a subject having endometriosis (by contacting a subject  
 CC with, or administering to subject, a nucleic acid molecule (II) that  
 CC modulates expression of VEGF, VEGFR1, and/or VEGFR2), a mammalian cell  
 CC (III) comprising (I) and administering to a mammal (I) (in conjunction  
 CC with a chemotherapeutic agent comprising contacting the mammal with the  
 CC compound and the chemotherapeutic agent under conditions suitable for the  
 CC administration). (I) is administered to a mammalian cell, preferably  
 CC human cell in the presence of a delivery reagent which is a lipid such as  
 CC cationic lipid or phospholipid, or a liposome. The enzymatic nucleic acid  
 CC molecule has an endonuclease activity to cleave RNA encoded by an VEGFR1  
 CC and/or VEGFR2 gene, and is in a hammerhead, inozyme, DNAzyme, G-cleaver,  
 CC or Amberzyme configuration. The enzymatic nucleic acids are useful for  
 CC inhibiting ocular angiogenesis associated with diabetic retinopathy or  
 CC age-related diabetic retinopathy, in a subject. They are also useful for  
 CC inhibiting angiogenesis, preferably tumor angiogenesis in cell, and for  
 CC treating a subject having a condition associated with an increased level  
 CC of VEGF receptor, where the condition is cancer, e.g. breast cancer, lung  
 CC cancer (such as non-small cell lung carcinoma), colorectal cancer, renal  
 CC cancer (such as renal cell carcinoma), pancreatic cancer. The enzymatic  
 CC nucleic acids are useful for treating a subject (preferably human) having  
 CC endometriosis, psoriasis, age-related macular degeneration, proliferative  
 CC diabetic retinopathy, hypoxia-induced angiogenesis, rheumatoid arthritis,  
 CC wound healing, endometrial carcinoma, gynecological bleeding disorders,  
 CC irregular menstrual cycles, ovulation, premenstrual syndrome, and  
 CC menopausal dysfunction. The enzymatic nucleic acids are useful for birth  
 CC control by inhibiting ovulation or embryonic uterine implantation. The  
 XX present sequence is a target sequence from the human VEGFR1/flt-1 mRNA.  
 XX  
 XX Sequence 17 BP; 2 A; 5 C; 5 G; 0 T; 5 U; 0 Other;



Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 64.3%; Pred. No. 86;  
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 26 CTCCTGGAGTCTCT 39  
 Db 2 CUCGGGAGUCCUCU 15

RESULT 79  
 ACN73127  
 ID ACN73127 standard; DNA; 17 BP.  
 XX AC  
 XX AC  
 XX AC  
 XX AC  
 DT 02-DEC-2004 (first entry)  
 XX Human GDMPLP-1 probe SEQ ID NO:10029.  
 XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX Homo sapiens.  
 OS  
 XX US2004137589-A1.  
 XX 15-JUL-2004.  
 XX 26-NOV-2003; 2003US-00723361.  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 PR 25-MAY-2001; 2001US-00866108.  
 XX (GUY/) GU Y.  
 PA (JTY/) JI Y.  
 PA (PENN/) PENN S G.  
 PA (HANZ/) HANZEL D K.  
 PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.  
 PA (SHAN/) SHANNON M E.  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 WPI; 2004-533378/51.  
 XX Novel myosin-like protein-1, useful for treating or preventing disorder  
 PT associated with decreased expression or activity of human genome-derived  
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 PT function.  
 XX Disclosure; SEQ ID NO 10029; Opp; English.  
 XX  
 XX  
 XX  
 CC The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or

CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 86;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 29 TGGAGTCTCTGAG 42  
 Db 1 TGGAGTCTCTGTG 14

RESULT 80  
 ADX59138  
 ID ADX59138 standard; DNA; 17 BP.  
 XX AC  
 XX AC  
 XX AC  
 XX ADX59138;  
 DT 21-APR-2005 (first entry)  
 XX Human liver cancer-associated gene promoter-related PCR primer SeqID107.  
 XX DNA methylation; promoter; liver tumor; PCR; primer; ss.  
 OS Homo sapiens.  
 XX CN1451759-A.  
 XX 29-OCT-2003.  
 XX 15-APR-2002; 2002CN-00111351.  
 XX 15-APR-2002; 2002CN-00111351.  
 XX (SHAN-) SHANGHAI INST ONCOLOGY.  
 XX Zhu J;  
 WPI; 2004-110093/12.  
 XX Methylation state of liver cancer related gene promoter CpG island and  
 PT its use in detecting liver cancer.  
 XX Claim 5; SEQ ID NO 107; 38pp; Chinese.  
 XX This invention relates to novel methylation state information about CpG  
 CC islands in the promoter region of a gene associated with primary liver  
 CC cancer, its use and a reagent kit for detecting primary liver cancer. The  
 CC reagent kit contains a methylation-specific restriction endonuclease and  
 CC the promoter CpG island-specific primer pairs of a gene associated with  
 CC liver cancer, a reagent for transforming the methylation cytosine to  
 CC uracil and primers for the promoter CpG island of the gene associated  
 CC with liver cancer. The present sequence is that of a PCR primer which was  
 CC for amplification of a region of a human liver cancer-associated gene  
 CC promoter during the analysis of methylation state in the exemplification  
 CC of the invention.  
 XX Sequence 17 BP; 7 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 16.1%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 86;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 AGAGCCAGCGAAGC 62  
 Db 2 AAAGCCAGCGAAGC 15

RESULT 81  
ADZ34403  
ID ADZ34403 standard; RNA; 17 BP.  
XX  
XX  
AC ADZ34403;  
XX  
XX 30-JUN-2005 (first entry)  
XX  
XX Human HER2 substrate RNA sequence SEQ ID NO:5441.  
DE  
XX short interfering RNA; siRNA; RNA interference; gene silencing;  
KW cytosolic; cancer; HER2; substrate; ss.  
XX  
XX Homo sapiens.  
XX  
XX US2005080031-A1.  
XX  
XX 14-APR-2005.  
XX  
XX 26-NOV-2003; 2003US-00724270.  
XX  
XX 18-MAY-2001; 2001US-0292217P.  
PR 29-MAY-2001; 2001US-0294140P.  
PR 06-JUN-2001; 2001US-0296249P.  
PR 20-JUL-2001; 2001US-0306883P.  
PR 13-AUG-2001; 2001US-0311865P.  
PR 10-SEP-2001; 2001US-0318471P.  
PR 20-FEB-2002; 2002US-0358580P.  
PR 06-MAR-2002; 2002US-0362016P.  
PR 11-MAY-2002; 2002US-0363124P.  
PR 29-MAY-2002; 2002US-0363124P.  
PR 29-MAY-2002; 2002US-0363124P.  
PR 06-JUN-2002; 2002US-0363124P.  
PR 06-JUN-2002; 2002US-0363124P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 10-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
PR 20-FEB-2003; 2003US-0440129P.  
PR 20-FEB-2003; 2003US-0440129P.  
PR 16-APR-2003; 2003US-04417012.  
PR 24-APR-2003; 2003US-04422704.  
PR 30-APR-2003; 2003US-04427160.  
PR 23-MAY-2003; 2003US-0444853.  
PR 29-AUG-2003; 2003US-04652791.  
PR 23-OCT-2003; 2003US-04652791.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
XX McSwiggen J;  
XX  
XX WPI; 2005-331166/34.  
XX  
XX Novel double-stranded short interfering RNA molecule having first  
PT nucleotide sequence complementary to RNA encoding HER2 or its portion,  
PT and second nucleotide sequence having complementarity to first sequence,  
PT useful for treating cancer.  
XX  
XX Example 10; SEQ ID NO 5441; 143pp; English.  
XX  
XX The invention relates to a double-stranded short interfering RNA (siRNA)  
CC molecule (I) comprising a first nucleotide sequence having 19-23  
CC nucleotides complementary to an RNA sequence encoding HER2 or its  
CC portion, and a second nucleotide sequence having 19-23 nucleotides  
CC exhibiting complementarity to the first sequence, and including at least  
CC one nucleotide that is not a 2'-OH containing ribonucleotide. Also  
CC described is a method of producing a class of nucleic acid-based gene  
CC modulating agents that exhibit a high degree of specificity for RNA of a  
CC desired target. (I) is useful for modulating HER2 activity in a cell, and  
CC for treating diseases or conditions related to levels of HER2 gene

CC expression. (I) is useful for treating cancer, such as pancreatic cancer,  
CC bladder cancer, lung cancer, breast cancer or prostate cancer. The  
CC present sequence represents a human HER2 substrate RNA sequence for a  
CC DNzyme (ribozyme), which is used in an example from the present  
CC invention for the identification of potential target sites in human HER2  
CC RNA.  
XX  
XX Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other;  
XX  
XX Query Match 16.1%; Score 12.4; DB 1; Length 17;  
XX Best Local Similarity 71.4%; Pred. No. 86;  
XX Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 28 CTGGAGTCTCTCTGA 41  
DB 4 CTGGAGCCCTCTCTGA 17  
RESULT 82  
AAA23004/C  
ID AAA23004 standard; RNA; 17 BP.  
XX  
XX AAA23004;  
XX  
XX 19-JUN-2000 (first entry)  
XX  
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:6230.  
XX  
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;  
KW ophthalmologic; antiinflammatory; antirheumatic; antiproliferative; ARMD;  
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
KW age related macular degeneration; inflammation; neovascular glaucoma;  
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;  
KW Kippel-Trenaunay-Weber syndrome; Oslar-Weber-Rendu syndrome; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9950403-A2.  
XX  
XX 07-OCT-1999.  
XX  
XX 24-MAR-1999; 99WO-US006507.  
XX  
XX 27-MAR-1998; 98US-0079678P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;  
XX WPI; 1999-591315/50.  
XX  
XX Novel ribozymes for modulating the synthesis, expression and/or stability  
PT of an mRNA encoding an angiogenic factors.  
XX  
XX Claim 54; Page 256; 305pp; English.  
XX  
XX The present invention describes enzymatic nucleic acid molecules with RNA  
CC cleaving activity, which specifically cleave RNA encoded by an aryl  
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
CC AAA21596 to AAA21688 represent their corresponding target sequences;  
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme  
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to

AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Oster-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3

Sequence 17 BP; 5 A; 7 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 15.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 92;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 16 GGGGATACAACTCTGGA 32  
Db 17 GGGGGTATTACTCTGGA 1

RESULT 83

ADV05926

ID ADV05926 standard; RNA; 17 BP.

AC ADV05926;

DT 10-FEB-2005 (first entry)

DE Human BACE DNzyme substrate sequence #192.

Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberyne; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human; ss.

Homo sapiens.

WO200116312-A2.

08-MAR-2001.

30-AUG-2000; 2000WO-US023998.

31-AUG-1999; 99US-0151713P.

27-SEP-1999; 99US-00406643.

27-SEP-1999; 99US-0156236P.

27-SEP-1999; 99US-0156467P.

06-NOV-1999; 99US-00436430.

08-DEC-1999; 99US-0169100P.

29-DEC-1999; 99US-00474432.

29-DEC-1999; 99US-0173612P.

30-DEC-1999; 99US-00476387.

04-FEB-2000; 2000US-00498824.

20-MAR-2000; 2000US-00531025.

14-APR-2000; 2000US-0197769P.

23-MAY-2000; 2000US-00578223.

09-AUG-2000; 2000US-00636385.

(RIBO-) RIBOZYME PHARM INC.

Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
Karpelaky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;

WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

Example 4; Page 380; 717pp; English.

The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyne, zinzyme, and/or DNzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for a DNzyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.

Sequence 17 BP; 2 A; 3 C; 8 G; 0 T; 4 U; 0 Other;

Query Match 15.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 58.8%; Pred. No. 92;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 61 GCTGATGTCCTGTCAAG 77  
Db 1 GCTGUGUGUCUGGCAAG 17

RESULT 84

ADV05024

ID ADV05024 standard; RNA; 17 BP.

AC ADV05024;

DT 10-FEB-2005 (first entry)

DE Human BACE zinzyme ribozyme substrate sequence #68.

Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberyne; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human; ss.

Homo sapiens.

WO200116312-A2.

08-MAR-2001.

30-AUG-2000; 2000WO-US023998.

31-AUG-1999; 99US-0151713P.

27-SEP-1999; 99US-00406643.

27-SEP-1999; 99US-0156236P.





CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX SQ Sequence 17 BP; 6 A; 2 C; 8 G; 0 T; 1 U; 0 Other;  
 Query Match 15.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 76.5%; Pred. No. 92;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 GACGGCCTGGGGATACA 24  
 || |||||  
 DB 1 GAAGGCCUGGGAAAGA 17

RESULT 88  
 ACN11559/C  
 ID ACN11559 standard; RNA; 17 BP.  
 XX ACN11559;  
 XX 22-APR-2004 (first entry)  
 XX WNV minus strand Inozyme substrate SEQ ID NO 11562.  
 XX WNV; West Nile Virus; antiinflammatory; cytotstatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX West Nile Virus.  
 OS  
 XX  
 PN W0200268637-A2.  
 XX  
 XX 06-SEP-2002.  
 XX  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX (BLAT/) BLATT L.  
 XX (MCSW/) MCSWIGGEN J A.  
 XX Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 XX Claim 23; SEQ ID NO 11562; 495pp; English.  
 XX  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX SQ Sequence 17 BP; 1 A; 8 C; 2 G; 0 T; 6 U; 0 Other;  
 Query Match 15.8%; Score 12.2; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 92;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 GACGGCCTGGGGATACA 24  
 || |||||  
 DB 17 GAAGGCCUGGGAAAGA 1

RESULT 89  
 ACA09006/C  
 ID ACA09006 standard; RNA; 17 BP.  
 XX ACA09006;  
 XX  
 XX 03-JUN-2003 (first entry)  
 XX NFKB sub-unit modulating amberzyme substrate #169.  
 XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyne;  
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;  
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 XX US2002177568-A1.  
 XX  
 XX 28-NOV-2002.  
 XX  
 XX 23-MAY-2001; 2001US-00864785.  
 XX  
 XX 07-DEC-1992; 92US-00987132.  
 XX 18-MAY-1994; 94US-00245466.  
 XX 15-AUG-1994; 94US-00291932.  
 XX 23-DEC-1996; 96US-00777916.  
 XX  
 XX (STIN/) STINCHCOMB D T.  
 XX (MCSW/) MCSWIGGEN J.  
 XX (DRAP/) DRAPER K G.  
 XX  
 XX Stinchcomb DT, Mcswiggen J, Draper KG;  
 XX WPI; 2003-340953/32.  
 XX  
 XX Novel enzymatic nucleic acid molecules which down regulates expression of  
 PT a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.  
 XX  
 XX Claim 3; Page 53; 72pp; English.  
 XX  
 XX The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFKB), where (I) is an inozyme, zinzyne, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,





RESULT 92  
 AEB61480/c  
 ID AEB61480 standard; mRNA; 17 BP.  
 XX  
 AC AEB61480;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human VEGF receptor 21 (Kdr) DNazyme target sequence SEQ ID 4058.  
 XX  
 KW VEGF receptor; angiogenesis; cancer; tumor; ocular disease;  
 KW diabetic retinopathy; age related macular degeneration;  
 KW angiogenesis disorder; rheumatoid arthritis; psoriasis; wound healing;  
 KW endometriosis; endometroid carcinoma; gynecological bleeding disorder;  
 KW menstruation disorder; premenstrual syndrome; menopause; Gynecological;  
 KW Cystostatic; Ophthalmological; Antidiabetic; antiangiogenic;  
 KW Antiproliferative; Antirheumatic; Antiarthritic; Vulnerary; Hemostatic;  
 KW Contraceptive; ss; enzymatic nucleic acid.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200296927-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 XX 29-MAY-2002; 2002WO-US017674.  
 XX  
 PR 29-MAY-2001; 2001US-00870161.  
 PR 30-NOV-2001; 2001US-033461P.  
 PR 03-MAY-2002; 2002US-00138674.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR ) CHIRON CORP.  
 PA  
 XX Escobedo J, Meswigen J, Pavco P, Stinchcomb D, Sandberg J;  
 PI Gordon G;  
 PI  
 XX WPI; 2003-140439/13.  
 DR  
 XX Novel enzymatic nucleic acids, ribozymes, which modulate expression of  
 PT genes encoding vascular endothelial growth factor and/or VEGF receptor,  
 PT useful for inhibiting tumor angiogenesis in cell, and for treating  
 PT cancer.  
 XX  
 PS Disclosure; SEQ ID NO 4058; 172pp; English.  
 XX  
 XX The invention relates to enzymatic nucleic acids (I) i.e.  
 CC ribozymes/DNAzymes/Zinzymes that target and modulate expression of, genes  
 CC encoding vascular endothelial growth factor (VEGF) and/or VEGF receptor  
 CC (VEGFR1 and 2 encode by the Flt-1 and Kdr genes respectively). Also  
 CC included are a composition comprising (I) and a carrier, administering  
 CC (I) to a cell (by contacting the cell with the compound under conditions  
 CC suitable for the administration), administering (I) to a cell (in  
 CC conjunction with one or more other drug by contacting the cell with the  
 CC compound and the other drug under conditions suitable for the  
 CC administration), administering (I) to a mammal (by contacting the mammal  
 CC with the compound under conditions suitable for the administration),  
 CC treating (M1) a subject having endometriosis (by contacting a subject  
 CC with, or administering to subject, a nucleic acid molecule (II) that  
 CC modulates expression of VEGF, VEGFR1, and/or VEGFR2), a mammalian cell  
 CC (III) comprising (I) and administering to a mammal (I) (in conjunction  
 CC with a chemotherapeutic agent comprising contacting the mammal with the  
 CC compound and the chemotherapeutic agent under conditions suitable for the  
 CC administration). (I) is administered to a mammalian cell, preferably  
 CC human cell in the presence of a delivery reagent which is a lipid such as  
 CC cationic lipid or phospholipid, or a liposome. The enzymatic nucleic acid  
 CC molecule has an endonuclease activity to cleave RNA encoded by an VEGFR1  
 CC and/or VEGFR2 gene, and is in a hammerhead, inozyme, DNazyme, G-cleaver,  
 CC or Ambzyme configuration. The enzymatic nucleic acids are useful for  
 CC inhibiting ocular angiogenesis associated with diabetic retinopathy or  
 CC age-related diabetic retinopathy, in a subject. They are also useful for  
 CC inhibiting angiogenesis, preferably tumor angiogenesis in cell, and for  
 CC treating a subject having a condition associated with an increased level

CC of VEGF receptor, where the condition is cancer, e.g. breast cancer, lung  
 CC cancer (such as non-small cell lung carcinoma), colorectal cancer, renal  
 CC cancer (such as renal cell carcinoma), pancreatic cancer. The enzymatic  
 CC nucleic acids are useful for treating a subject (preferably human) having  
 CC endometriosis, psoriasis, age-related macular degeneration, proliferative  
 CC diabetic retinopathy, hypoxia-induced angiogenesis, rheumatoid arthritis,  
 CC wound healing, endometrial carcinoma, gynecologic bleeding disorders,  
 CC irregular menstrual cycles, ovulation, premenstrual syndrome, and  
 CC menopausal dysfunction. The enzymatic nucleic acids are useful for birth  
 CC control by inhibiting ovulation or embryonic uterine implantation. The  
 CC present sequence is a target sequence from the human VEGFR2/Kdr mRNA.  
 XX  
 SQ Sequence 17 BP; 7 A; 4 C; 3 G; 0 T; 3 U; 0 Other;  
 Query Match 15.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 92;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 60 AGCTGATGCTCTGTCAA 76  
 DB |||||  
 17 AGTTGCTGTGTCAA 1  
 RESULT 93  
 ADX84037  
 ID ADX84037 standard; DNA; 17 BP.  
 XX  
 AC ADX84037;  
 XX  
 DT 05-MAY-2005 (first entry)  
 XX  
 DE DNA detection extension primer #36.  
 XX  
 KW Analysis; mass spectroscopy; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005014850-A2.  
 XX  
 PD 17-FEB-2005.  
 XX  
 PF 06-AUG-2004; 2004WO-US025526.  
 XX  
 PR 06-AUG-2003; 2003US-0493238P.  
 PR 07-MAY-2004; 2004US-0568958P.  
 XX  
 XX (UYMA-) UNIV MASSACHUSETTS.  
 PA  
 XX Ginns EI, Galdzicka M;  
 XX  
 DR WPI; 2005-195764/20.  
 XX  
 XX Clinical assay system for assaying sample, has central controller, sample  
 PT transfer module, nucleic acid extraction and measurement module,  
 PT thermocycling module, primer extension module, mass spectrometry module  
 PT analyzing sample.  
 XX  
 XX Claim 6; SEQ ID NO 108; 207pp; English.  
 PS  
 XX The invention relates to a system for performing an assay on a biological  
 CC sample, comprising a central controller programmed to exchange  
 CC information about the biological sample with an outside system or  
 CC database and exchange information about the biological sample with one or  
 CC more modules of the system, a sample transfer module for transferring a  
 CC portion of the sample to a first container, a nucleic acid extraction  
 CC module for extracting nucleic acids from cells within the portion and for  
 CC transferring the portion from the first container to a second container,  
 CC a nucleic acid measurement module for measuring the concentration of  
 CC nucleic acids in the portion, a PCR preparation module for adding PCR  
 CC reaction materials to the portion, a thermocycling module for amplifying  
 CC a target sequence and extending a primer in the portion, a primer  
 CC extension preparation module for adding primer extension reaction  
 CC materials to the portion, a mass spectrometry preparation module for



CC removing a sample of the portion from the second container to a support  
 CC for analysis by mass spectrometry and a mass spectrometry module for  
 CC analyzing the sample. The invention also relates to an automated method  
 CC for detecting mutations in a target gene. The diagnostic assay is an  
 CC assay for detecting a pathogen in the sample. The pathogen is a virus,  
 CC bacterium or fungus. The virus is a virus of the family Herpesviridae,  
 CC preferably Cytomegalovirus (CMV). The system enables high accurate assays  
 CC on nucleic acid sequences (e.g. clinically relevant nucleic acid  
 CC sequences) using mass spectrometry. This sequence represents a DNA  
 CC detection extension primer used in the scope of the invention.

XX SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 15.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 92;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 25 ACTCTGGAGTCTCTGA 41

Db 1 ACACAGGCGTCTCTGA 17

#### RESULT 94

ADM56305/C  
 ID ADM56305 standard; DNA; 12 BP.

XX AC ADM56305;

XX 03-JUN-2004 (first entry)

XX DE Mouse SLC26A6 anion transporter protein gene splice site #24.

XX SLC26A6; SLC26A1; SLC26A2; anion transporter protein; cancer;

XX splice site; ds; mouse; murine.

XX OS Mus musculus.

XX PN WO2003072759-A2.

XX PD 04-SEP-2003.

XX PP 28-FEB-2003; 2003WO-US006469.

XX PR 28-FEB-2002; 2002US-0360275P.

XX (UYVA-) UNIV VANDERBILT.

XX PA (UYCA-) UNIV CASE WESTERN RESERVE.

XX PA (SGHM) BRIGHAM & WOMENS HOSPITAL.

XX Mount DB, Romero MF;

XX WPI; 2003-712726/67.

XX New SLC26A6, SLC26A1 or SLC26A2 polypeptide, useful for preparing a

XX composition for treating e.g., cancer.

XX Example 2; SEQ ID NO 37; 204pp; English.

XX The invention comprises the amino acid and coding sequences of SLC26A6,  
 CC SLC26A1 and SLC26A2 anion transporter proteins. The DNA and protein  
 CC sequences of the invention are useful for treating cancer. The present  
 CC DNA sequence represents a splice site from the gene encoding the mouse  
 CC SLC26A6 anion transporter protein.

XX SQ Sequence 12 BP; 1 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 15.6%; Score 12; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 67;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GACGGCCTGGGG 19

Db 12 GACGGCCTGGGG 1

#### RESULT 95

ADR70044

ID ADR70044 standard; DNA; 16 BP.

XX AC ADR70044;

XX 04-NOV-2004 (first entry)

XX Human survivin gene modulatory oligonucleotide #112.

XX ss; antiangiogenic; cytostatic; antiarteriosclerotic; antipsoriatic;  
 KW antidiabetic; ophthalmological; antiarthritic; antirheumatic;  
 KW antiaesthetic; antiallergic; antiinflammatory; dermatological; anti-HIV;  
 KW virucide; survivin antagonist; apoptosis inhibitor;  
 KW cellular proliferation inhibitor; survivin; gene expression;  
 KW abnormal angiogenesis; chemotherapeutic agent; busulfan; myleran;  
 KW carboplatin; paraplatin; Taxol; doxorubicin; adriamycin; atherosclerosis;  
 KW psoriasis; diabetic retinopathy; rheumatoid arthritis; asthma; warts;  
 KW allergic dermatitis; cancer; tumour; sarcoma; glioma; carcinoma;  
 KW melanoma; osteosarcoma; Swing's sarcoma; chondrosarcoma;  
 KW malignant fibrous histiocytoma; fibrosarcoma; Kaposi's sarcoma;  
 KW Paclitaxel; Docetaxel.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1..16

FT /\*tag= b

FT /mod\_base= OTHER

FT /note= "OTHER = phosphorothioate internucleotide

linkages, all locked nucleic acid (LNA) residues are 5'-

FT modified\_base 1..4

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "OTHER = beta-D-oxy-locked nucleic acid but

optionally DNA nucleotides, optionally phosphate

FT internucleotide linkages"

FT modified\_base 13..16

FT /\*tag= c

FT /mod\_base= OTHER

FT /note= "OTHER = beta-D-oxy-locked nucleic acid but

optionally DNA nucleotides, optionally phosphate

FT internucleotide linkages"

XX WO2004069991-A2.

XX 19-AUG-2004.

XX 10-FEB-2004; 2004WO-DK000096.

XX 10-FEB-2003; 2003DK-00000183.

XX 18-NOV-2003; 2003DK-00001708.

XX (SANT-) SANTARIS PHARMA AS.

XX Hansen B, Thru CH, Petersen KD, Westergaard M, Wissenbach M;

XX WPI; 2004-625494/60.

XX New locked nucleic acid containing oligomeric compound capable of  
 PT modulating survivin expression, useful for treating cancer such as breast  
 PT carcinoma, lung carcinoma, etc.

XX Claim 1; SEQ ID NO 113; 122pp; English.

XX The invention relates to an oligomeric compound (I) capable of modulating  
 CC survivin expression, having 8-50 nucleotides and/or nucleotide analogues,  
 CC where the compound comprises a subsequence of at least 8 nucleotides or  
 CC nucleotide analogues, where the subsequence is located within a sequence

CC chosen from one of 143 sequences given in the specification. (I) is  
 CC useful for treating a mammal suffering from or susceptible from a disease  
 CC caused by abnormal angiogenesis, by administering (I) containing one or  
 CC more LNA units that are targeted to survivin. (II) is useful as a  
 CC medicament and for the manufacture of a medicament for the treatment of  
 CC cancer, in combination with chemotherapeutic agent such as busulfan  
 CC (myleran), carboplatin (paraplatin), Taxol, doxorubicin (adriamycin),  
 CC etc. (I) or a conjugate (II) containing (I) is useful in the preparation  
 CC of a medicament for the treatment of atherosclerosis, psoriasis, diabetic  
 CC retinopathy, rheumatoid arthritis, asthma, warts and allergic dermatitis.  
 CC (I), (II) or a pharmaceutical (III) containing (I) is useful for treating  
 CC cancer in the form of a solid tumour, sarcoma, glioma or carcinoma chosen  
 CC from malignant melanoma, basal cell carcinoma, ovarian carcinoma, breast  
 CC carcinoma, non-small cell lung cancer, renal cell carcinoma, bladder  
 CC carcinoma, recurrent superficial bladder cancer, stomach carcinoma,  
 CC prostatic carcinoma, pancreatic carcinoma, lung carcinoma, cervical  
 CC carcinoma, cervical dysplasia, laryngeal papillomatosis, colon carcinoma,  
 CC colorectal carcinoma and carcinoma tumours. The malignant melanoma is  
 CC chosen from superficial spreading melanoma, nodular melanoma, lentigo  
 CC maligna melanoma, acral melanoma, amelanotic melanoma, and desmoplastic  
 CC melanoma. The sarcoma is chosen from osteosarcoma, Ewing's sarcoma,  
 CC chondrosarcoma, malignant fibrous histiocytoma, fibrosarcoma and Kaposi's  
 CC sarcoma. The treatment further involves administration of a  
 CC chemotherapeutic agent such as taxanes, preferably Taxol, Paclitaxel or  
 CC Docetaxel. (I), (II) or (III) is also useful for preventing or limiting  
 CC apoptosis or for preventing cellular proliferation. This sequence  
 CC corresponds to an antisense oligonucleotide targeted to the human  
 CC survivin gene.

XX SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 15.6%; Score 12; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGGAAGCTG 64

Db 4 CCAGCGGAAGCTG 15

RESULT 96

ADW10034

ID ADW10034 standard; DNA; 16 BP.

AC ADW10034;

DT 07-APR-2005 (first entry)

XX Human survivin antisense oligonucleotide 113A, SEQ ID NO:592.

XX Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;  
 KW basal cell carcinoma; ovary tumor; breast tumor;  
 KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;  
 KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;  
 KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;  
 KW sarcoma; osteosarcoma; Kaposi's sarcoma; anti-HIV; glioma; cytostatic;  
 KW endocrine disease; gynecology and obstetrics; genitourinary disease;  
 KW respiratory disease; musculoskeletal disease; dermatological disease;  
 KW proliferative disorder; atherosclerosis; antiarteriosclerotic;  
 KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;  
 KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;  
 KW cardiovascular disease; ocular disease; rheumatoid arthritis;  
 KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;  
 KW skin allergy; antiallergic; antiinflammatory; dermatological;  
 KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;  
 KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;  
 KW antisense oligonucleotide; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT misc\_binding 1..16

FT /\*tag= b

FT /bound moiety= "Bases 1568-1553 of human survivin cDNA  
 FT (SEQ ID NO:1)"  
 FT modified\_base 1..16  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate linkages"  
 FT modified\_base 1..4  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Beta-D-oxy-LNAs (locked nucleic acid). All beta-D-  
 FT -oxy-LNA cytosines are 5-methylcytosine"  
 FT modified\_base 13..16  
 FT /\*tag= d  
 FT /mod\_base= OTHER  
 FT /note= "Beta-D-oxy-LNAs. All beta-D-oxy-LNA cytosines are  
 FT 5-methylcytosine"

US2005014712-A1.

20-JAN-2005.

10-FEB-2004; 2004US-00776934.

10-FEB-2003; 2003US-0446372P.

19-NOV-2003; 2003US-0523591P.

(HANS/) HANSEN B.

(THRU/) THRU C A.

(WEST/) WESTERGAARD M.

(PETE/) PETERSEN K D.

(WISS/) WISSENBACH M.

Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;

WPI; 2005-100663/11.

XX New oligomeric compound for the modulation of survivin, useful for  
 PT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,  
 PT rheumatoid arthritis, asthma, warts, or allergic dermatitis.

PS Example 10; SEQ ID NO 592; 264pp; English.

XX The invention relates to antisense oligonucleotides consisting of 8-50  
 CC nucleotides and/or nucleotide analogs which inhibit expression of human  
 CC survivin, an inhibitor of apoptosis which is also essential for cell  
 CC division and angiogenesis. The antisense oligonucleotides comprise a  
 CC subsequence of 8 or more nucleotides or nucleotide analogs wherein the  
 CC subsequence is located within a sequence selected from ADW09444-ADW09586.  
 CC The oligonucleotides preferably contain one or more (preferably 6-10)  
 CC nucleotide analogs, especially a locked nucleic acid (LNA), and also  
 CC preferably contain a linkage group selected from a phosphate group, a  
 CC phosphorothioate group or a boranophosphate group. The invention also  
 CC relates to a conjugate comprising a survivin antisense oligonucleotide of  
 CC the invention and one or more non-nucleotide or non-polynucleotide  
 CC moieties covalently attached to the oligonucleotide; and a pharmaceutical  
 CC composition comprising a survivin antisense oligonucleotide or conjugate  
 CC of the invention, optionally further comprising a chemotherapeutic agent.  
 CC The survivin antisense oligonucleotides, and conjugates and compositions  
 CC containing them, are useful in the treatment of cancers such as  
 CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian  
 CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell  
 CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer, lung  
 CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung  
 CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal  
 CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma  
 CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,  
 CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or  
 CC gliomas. The survivin antisense oligonucleotides are also useful in the  
 CC treatment of conditions such as atherosclerosis, psoriasis, diabetic  
 CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic  
 CC dermatitis. They may additionally be used for inhibiting cellular  
 CC proliferation, for modulating apoptosis and for treating a disease  
 CC related to abnormal angiogenesis. The survivin antisense oligonucleotides

CC of the invention are shorter than prior art survivin antisense  
 CC oligonucleotides (16-mers compared to 20-25-mers), therefore having  
 CC increased specificity and affinity for survivin mRNA, and also have  
 CC higher biostability and cell permeability. The present sequence  
 CC represents an antisense oligonucleotide targeted to the human survivin  
 CC cDNA target sequence shown in ADW09443 used in an example of the  
 CC invention.

XX  
 SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 15.6%; Score 12; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 53 CCACGCGAAGCTG 64  
 |||||  
 Db 4 CCACGCGAAGCTG 15

RESULT 97  
 ADW09555  
 ID ADW09555 standard; DNA; 16 BP.  
 AC ADW09555;  
 XX  
 DT 07-APR-2005 (first entry)  
 XX  
 DE Human survivin antisense oligonucleotide, SEQ ID NO:113.  
 XX  
 KW Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;  
 KW basal cell carcinoma; ovary tumor; breast tumor;  
 KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;  
 KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;  
 KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;  
 KW sarcoma; osteosarcoma; Kaposi's sarcoma; anti-HIV; glioma; cytostatic;  
 KW endocrine disease; gynecology and obstetrics; genitourinary disease;  
 KW respiratory disease; musculoskeletal disease; dermatological disease;  
 KW proliferative disorder; atherosclerosis; antiarteriosclerotic;  
 KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;  
 KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;  
 KW cardiovascular disease; ocular disease; rheumatoid arthritis;  
 KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;  
 KW skin allergy; antiallergic; antiinflammatory; dermatological;  
 KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;  
 KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;  
 KW antisense oligonucleotide; ss.  
 XX  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers  
 FT misc\_binding 1..16  
 FT /tag= c  
 FT /bound\_molety= "Bases 1568-1553 of human survivin cDNA  
 FT (SEQ ID NO:1)"  
 FT modified\_base 1..5  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "Optionally phosphorothioate linkages when  
 FT nucleotides 1-4 are beta-D-oxy-LNA. When nucleotides 1-4  
 FT are unmodified, the internucleotide linkages are  
 FT phosphorothioate"  
 FT modified\_base 1..4  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Optionally beta-D-oxy-LNAs (locked nucleic acid).  
 FT All beta-D-oxy-LNA cytosines are 5-methylcytosine"  
 FT modified\_base 5..13  
 FT /tag= d  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate linkages"  
 FT modified\_base 13..15  
 FT /tag= e  
 FT /mod\_base= OTHER

FT /note= "Optionally beta-D-oxy-LNAs. All beta-D-oxy-LNA  
 FT cytosines are 5-methylcytosine. Optionally  
 FT phosphorothioate linkages when bases 13-15 are beta-D-oxy  
 FT -LNAs. When nucleotides 13-15 are unmodified, the  
 FT internucleotide linkages are phosphorothioate"  
 FT modified\_base 15..16  
 FT /tag= f  
 FT /mod\_base= OTHER  
 FT /note= "Optionally phosphorothioate linkage when  
 FT nucleotide 16 is beta-D-oxy-LNA. This linkage is  
 FT phosphorothioate when nucleotide 16 is unmodified"  
 FT modified\_base 16  
 FT /tag= g  
 FT /mod\_base= OTHER  
 FT /note= "Optionally beta-D-oxy-LNA. When this nucleotide  
 FT is unmodified, the linkage between nucleotides 15 and 16  
 FT is phosphorothioate"  
 XX  
 PN US2005014712-A1.  
 XX  
 XX 20-JAN-2005.  
 XX  
 XX 10-FEB-2004; 2004US-00776934.  
 XX  
 XX 10-FEB-2003; 2003US-0446372P.  
 PR 19-NOV-2003; 2003US-0523591P.  
 XX  
 XX (HANS// HANSEN B.  
 PA (THRU// THRU C A.  
 PA (WEST// WESTERGAARD M.  
 PA (PETE// PETERSEN K D.  
 PA (WISS// WISSENBACH M.  
 XX  
 XX Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;  
 WI; 2005-100663/11.  
 DR  
 XX New oligomeric compound for the modulation of survivin, useful for  
 FT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,  
 FT rheumatoid arthritis, asthma, warts, or allergic dermatitis.  
 XX  
 PS Claim 1; SEQ ID NO 113; 264pp; English.  
 XX  
 CC The invention relates to antisense oligonucleotides consisting of 8-50  
 CC nucleotides and/or nucleotide analogs which inhibit expression of human  
 CC survivin, an inhibitor of apoptosis which is also essential for cell  
 CC division and angiogenesis. The antisense oligonucleotides comprise a  
 CC subsequence of 8 or more nucleotides or nucleotide analogs wherein the  
 CC subsequence is located within a sequence selected from ADW09444-ADW09586.  
 CC The oligonucleotides preferably contain one or more (preferably 6-10)  
 CC nucleotide analogs, especially a locked nucleic acid (LNA), and also  
 CC preferably contain a linkage group selected from a phosphate group, a  
 CC phosphorothioate group or a boranophosphate group. The invention also  
 CC relates to a conjugate comprising a survivin antisense oligonucleotide of  
 CC the invention and one or more non-nucleotide or non-poly-nucleotide  
 CC moieties covalently attached to the oligonucleotide; and a pharmaceutical  
 CC composition comprising a survivin antisense oligonucleotide or conjugate  
 CC of the invention, optionally further comprising a chemotherapeutic agent.  
 CC The survivin antisense oligonucleotides, and conjugates and compositions  
 CC containing them, are useful in the treatment of cancers such as  
 CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian  
 CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell  
 CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,  
 CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung  
 CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma  
 CC tumors); sarcomas (e.g., osteosarcoma, Kaposi's sarcoma, chondrosarcoma,  
 CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or  
 CC gliomas. The survivin antisense oligonucleotides are also useful in the  
 CC treatment of conditions such as atherosclerosis, psoriasis, diabetic  
 CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic  
 CC dermatitis. They may additionally be used for inhibiting cellular  
 CC proliferation, for modulating apoptosis and for treating a disease

CC related to abnormal angiogenesis. The survivin antisense oligonucleotides  
 CC of the invention are shorter than prior art survivin antisense  
 CC oligonucleotides (16-mers compared to 20-25-mers), therefore having  
 CC increased specificity and affinity for survivin mRNA, and also have  
 CC higher biostability and cell permeability. The present sequence  
 CC represents a specifically claimed antisense oligonucleotide targeted to  
 CC the human survivin cDNA target sequence shown in ADM09443.

XX  
 SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 15.6%; Score 12; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 CCAGCGAAGCTG 64  
 |||||  
 Db 4 CCAGCGAAGCTG 15

RESULT 98  
 ADM10035  
 ID ADM10035 standard; DNA; 16 BP.  
 XX  
 AC ADM10035;  
 XX  
 DT 07-APR-2005 (first entry)  
 XX  
 DE Human survivin antisense oligonucleotide 113B, SEQ ID NO:593.

XX Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;  
 KW basal cell carcinoma; ovary tumor; breast tumor;  
 KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;  
 KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;  
 KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;  
 KW sarcoma; osteosarcoma; Kaposi's sarcoma; anti-HIV; glioma; cytostatic;  
 KW endocrine disease; gynecology and obstetrics; genitourinary disease;  
 KW respiratory disease; musculoskeletal disease; dermatological disease;  
 KW proliferative disorder; atherosclerosis; antiarteriosclerotic;  
 KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;  
 KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;  
 KW cardiovascular disease; ocular disease; rheumatoid arthritis;  
 KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;  
 KW skin allergy; antiallergic; antiinflammatory; dermatological;  
 KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;  
 KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;  
 XX antisense oligonucleotide; ss.

OS Homo sapiens.

XX  
 FH Key Location/Qualifiers  
 FT misc\_binding 1..16  
 FT /tag= b  
 FT /bound moiety= "Bases 1568-1553 of human survivin cDNA  
 FT (SEQ ID NO:1)"  
 FT modified\_base 1..16  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate linkages"  
 FT modified\_base 1..4  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Beta-D-oxy-LNAs (locked nucleic acid). All beta-D  
 FT -oxy-LNA cytosines are 5-methylcytosine"  
 FT modified\_base 13..15  
 FT /tag= d  
 FT /mod\_base= OTHER  
 FT /note= "Beta-D-oxy-LNAs. All beta-D-oxy-LNA cytosines are  
 FT 5-methylcytosine"  
 XX  
 FN US2005014712-A1.  
 XX  
 PD 20-JAN-2005.  
 XX

PF 10-FEB-2004; 2004US-00776934.  
 XX  
 PR 10-FEB-2003; 2003US-0446372P.  
 PR 19-NOV-2003; 2003US-0523591P.  
 XX  
 PA (HANS/) HANSEN B.  
 PA (THRU/) THRU C A.  
 PA (WEST/) WESTERGAARD M.  
 PA (PETE/) PETERSEN K D.  
 PA (WISS/) WISSENBACH M.

XX Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;  
 PI WPI; 2005-100663/11.  
 XX  
 DR  
 XX  
 XX New oligomeric compound for the modulation of survivin, useful for  
 PT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,  
 PT rheumatoid arthritis, asthma, warts, or allergic dermatitis.  
 XX  
 PS Example 10; SEQ ID NO 593; 264pp; English.

XX The invention relates to antisense oligonucleotides consisting of 8-50  
 CC nucleotides and/or nucleotide analogs which inhibit expression of human  
 CC survivin, an inhibitor of apoptosis which is also essential for cell  
 CC division and angiogenesis. The antisense oligonucleotides comprise a  
 CC subsequence of 8 or more nucleotides or nucleotide analogs, wherein the  
 CC subsequence is located within a sequence selected from ADM09444-ADM09586.  
 CC The oligonucleotides preferably contain one or more (preferably 6-10)  
 CC nucleotide analogs, especially a locked nucleic acid (LNA), and also  
 CC preferably contain a linkage group selected from a phosphate group, a  
 CC phosphorothioate group or a boranophosphate group. The invention also  
 CC relates to a conjugate comprising a survivin antisense oligonucleotide of  
 CC the invention and one or more non-nucleotide or non-polynucleotide  
 CC moieties covalently attached to the oligonucleotide; and a pharmaceutical  
 CC composition comprising a survivin antisense oligonucleotide or conjugate  
 CC of the invention, optionally further comprising a chemotherapeutic agent.  
 CC The survivin antisense oligonucleotides, and conjugates and compositions  
 CC containing them, are useful in the treatment of cancers such as  
 CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian  
 CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell  
 CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,  
 CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung  
 CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal  
 CC papillomatosis, colon carcinoma, colorectal carcinoma, and carcinoid  
 CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,  
 CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or  
 CC gliomas. The survivin antisense oligonucleotides are also useful in the  
 CC treatment of conditions such as atherosclerosis, psoriasis, diabetic  
 CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic  
 CC dermatitis. They may additionally be used for inhibiting cellular  
 CC proliferation, for modulating apoptosis and for treating a disease  
 CC related to abnormal angiogenesis. The survivin antisense oligonucleotides  
 CC of the invention are shorter than prior art survivin antisense  
 CC oligonucleotides (16-mers compared to 20-25-mers), therefore having  
 CC increased specificity and affinity for survivin mRNA, and also have  
 CC higher biostability and cell permeability. The present sequence  
 CC represents an antisense oligonucleotide targeted to the human survivin  
 CC cDNA target sequence shown in ADM09443 used in an example of the  
 CC invention.

XX  
 SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 15.6%; Score 12; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 CCAGCGAAGCTG 64  
 |||||  
 Db 4 CCAGCGAAGCTG 15

RESULT 99  
 ADM10037

ID ADW10037 standard; DNA; 16 BP.  
AC ADW10037;  
XX 07-APR-2005 (first entry)  
XX Human survivin antisense oligonucleotide 113D, SEQ ID NO:595.  
XX Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;  
KW basal cell carcinoma; ovary tumor; breast tumor;  
KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;  
KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;  
KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;  
KW sarcoma; osteosarcoma; Kaposi's sarcoma; anti-HIV; glioma; cytostatic;  
KW endocrine disease; gynecology and obstetrics; genitourinary disease;  
KW respiratory disease; musculoskeletal disease; dermatological disease;  
KW proliferative disorder; atherosclerosis; antiarteriosclerotic;  
KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;  
KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;  
KW cardiovascular disease; ocular disease; rheumatoid arthritis;  
KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;  
KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;  
KW angiogenesis disorder; survivin; phosphorothioate;  
XX antisense oligonucleotide; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX misc\_binding 1..16 /\*tag= a  
FT /bound\_moiety= "Bases 1568-1553 of human survivin cDNA  
FT (SEQ ID NO:1)"  
FT modified\_base 1..16 /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate linkages"  
XX  
XX US2005014712-A1.  
XX  
XX 20-JAN-2005.  
XX  
XX 10-FEB-2004; 2004US-00776934.  
XX  
XX 10-FEB-2003; 2003US-0446372P.  
XX 19-NOV-2003; 2003US-0523591P.  
XX  
XX (HANS/) HANSEN B.  
XX (THRU/) THRU C A.  
XX (WEST/) WESTERGAARD M.  
XX (PETE/) PETERSEN K D.  
XX (WISS/) WISSENBACH M.  
XX  
XX Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;  
XX WPI; 2005-100663/11.  
XX  
XX New oligomeric compound for the modulation of survivin, useful for  
XX treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,  
XX rheumatoid arthritis, asthma, warts, or allergic dermatitis.  
XX  
XX Example 10; SEQ ID NO 595; 264pp; English.  
XX  
XX The invention relates to antisense oligonucleotides consisting of 8-50  
XX nucleotides and/or nucleotide analogs which inhibit expression of human  
XX survivin, an inhibitor of apoptosis which is also essential for cell  
XX division and angiogenesis. The antisense oligonucleotides comprise a  
XX subsequence of 8 or more nucleotides or nucleotide analogs, wherein the  
XX subsequence is located within a sequence selected from ADW09444-ADW09586.  
XX The oligonucleotides preferably contain one or more (preferably 6-10)  
XX nucleotide analogs, especially a locked nucleic acid (LNA), and also  
XX preferably contain a linkage group selected from a phosphate group, a  
XX phosphorothioate group or a boranophosphate group. The invention also

CC relates to a conjugate comprising a survivin antisense oligonucleotide of  
CC the invention and one or more non-nucleotide or non-polynucleotide  
CC moieties covalently attached to the oligonucleotide; and a pharmaceutical  
CC composition comprising a survivin antisense oligonucleotide or conjugate  
CC of the invention, optionally further comprising a chemotherapeutic agent.  
CC The survivin antisense oligonucleotides, and conjugates and compositions  
CC containing them, are useful in the treatment of cancers such as  
CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian  
CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell  
CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,  
CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung  
CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal  
CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma  
CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,  
CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or  
CC gliomas. The survivin antisense oligonucleotides are also useful in the  
CC treatment of conditions such as atherosclerosis, psoriasis, diabetic  
CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic  
CC dermatitis. They may additionally be used for inhibiting cellular  
CC proliferation, for modulating apoptosis and for treating a disease  
CC related to abnormal angiogenesis. The survivin antisense oligonucleotides  
CC of the invention are shorter than prior art survivin antisense  
CC oligonucleotides (16-mers compared to 20-25-mers), therefore having  
CC increased specificity and affinity for survivin mRNA, and also have  
CC higher biostability and cell permeability. The present sequence  
CC represents an antisense oligonucleotide targeted to the human survivin  
CC cDNA target sequence shown in ADW09443 used in an example of the  
CC invention.  
XX SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 15.6%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 53 CCAGCGAAGCTG 64  
DB |||||  
4 CCAGCGAAGCTG 15  
RESULT 100  
ADW10036  
ID ADW10036 standard; DNA; 16 BP.  
XX  
XX AC ADW10036;  
XX 07-APR-2005 (first entry)  
XX Human survivin antisense oligonucleotide 113C, SEQ ID NO:594.  
XX Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;  
KW basal cell carcinoma; ovary tumor; breast tumor;  
KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;  
KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;  
KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;  
KW sarcoma; osteosarcoma; Kaposi's sarcoma; anti-HIV; glioma; cytostatic;  
KW endocrine disease; gynecology and obstetrics; genitourinary disease;  
KW respiratory disease; musculoskeletal disease; dermatological disease;  
KW proliferative disorder; atherosclerosis; antiarteriosclerotic;  
KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;  
KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;  
KW cardiovascular disease; ocular disease; rheumatoid arthritis;  
KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;  
KW skin allergy; antiallergic; antiinflammatory; dermatological;  
KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;  
KW angiogenesis disorder; survivin; phosphorothioate; ss.  
XX antisense oligonucleotide; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX misc\_binding 1..16 /\*tag= b

FT /bound moiety= "Bases 1568-1553 of human survivin cDNA  
 (SEQ ID NO:1)"  
 FT 1..4  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Beta-D-oxo-LNAs (locked nucleic acid). All beta-D-  
 FT -oxy-LNA cytosines are 5-methylcytosine"  
 FT 5..13  
 FT /modified\_base  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate linkages"  
 FT 13..16  
 FT /modified\_base  
 FT /\*tag= d  
 FT /mod\_base= OTHER  
 FT /note= "Beta-D-oxo-LNAs. All beta-D-oxo-LNA cytosines are  
 FT 5-methylcytosine"  
 XX US2005014712-A1.  
 XX 20-JAN-2005.  
 XX 10-FEB-2004; 2004US-00776934.  
 XX 10-FEB-2003; 2003US-0446372P.  
 PR 19-NOV-2003; 2003US-0523591P.  
 XX  
 PA (HANS/) HANSEN B.  
 PA (THRU/) THRU C.A.  
 PA (WEST/) WESTERGAARD M.  
 PA (PETE/) PETERSEN K D.  
 PA (WISS/) WISSENBACH M.  
 XX Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;  
 XX WPI; 2005-100663/11.  
 XX  
 XX New oligomeric compound for the modulation of survivin, useful for  
 PT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,  
 PT rheumatoid arthritis, asthma, warts, or allergic dermatitis.  
 XX  
 PS Example 10; SEQ ID NO 594; 264pp; English.

XX The invention relates to antisense oligonucleotides consisting of 8-50  
 CC nucleotides and/or nucleotide analogs which inhibit expression of human  
 CC survivin, an inhibitor of apoptosis which is also essential for cell  
 CC division and angiogenesis. The antisense oligonucleotides comprise a  
 CC subsequence of 8 or more nucleotides or nucleotide analogs, wherein the  
 CC subsequence is located within a sequence selected from ADM09444-ADM09586.  
 CC The oligonucleotides preferably contain one or more (preferably 6-10)  
 CC nucleotide analogs, especially a locked nucleic acid (LNA), and also  
 CC preferably contain a linkage group selected from a phosphate group, a  
 CC phosphorothioate group or a boranophosphate group. The invention also  
 CC relates to a conjugate comprising a survivin antisense oligonucleotide of  
 CC the invention and one or more non-nucleotide or non-polynucleotide  
 CC moieties covalently attached to the oligonucleotide; and a pharmaceutical  
 CC composition comprising a survivin antisense oligonucleotide or conjugate  
 CC of the invention, optionally further comprising a chemotherapeutic agent.  
 CC The survivin antisense oligonucleotides, and conjugates and compositions  
 CC containing them, are useful in the treatment of cancers such as  
 CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian  
 CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell  
 CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,  
 CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung  
 CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal  
 CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma  
 CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,  
 CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or  
 CC gliomas. The survivin antisense oligonucleotides are also useful in the  
 CC treatment of conditions such as atherosclerosis, psoriasis, diabetic  
 CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic  
 CC dermatitis. They may additionally be used for inhibiting cellular  
 CC proliferation, for modulating apoptosis and for treating a disease  
 CC related to abnormal angiogenesis. The survivin antisense oligonucleotides

CC of the invention are shorter than prior art survivin antisense  
 CC oligonucleotides (16-mers compared to 20-25-mers), therefore having  
 CC increased specificity and affinity for survivin mRNA, and also have  
 CC higher biostability and cell permeability. The present sequence  
 CC represents an antisense oligonucleotide targeted to the human survivin  
 CC cDNA target sequence shown in ADM09443 used in an example of the  
 CC invention.  
 XX SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 15.6%; Score 12; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred.No. 92;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 53 CCAGCGAAGCTG 64  
 DB 4 CCAGCGAAGCTG 15  
 |||||  
 RESULT 101  
 ABN10030  
 ID ABN10030 standard; DNA; 17 BP.  
 XX  
 AC ABN10030;  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10022.  
 XX  
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192524-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 25-MAY-2001; 2001WO-US016981.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 05-FEB-2001; 2001WO-US000670.  
 XX  
 XX (AEOM-) AEOMICA INC.  
 PA  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 PI WPI; 2002-179446/23.  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX  
 PS Disclosure; SEQ ID NO 10022; 214pp; English.  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify



CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 15.6%; Score 12; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 98;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCCTC 38  
 Db 6 TCTGGAGTCCTC 17

RESULT 102  
 ACN73120  
 ID ACN73120 standard; DNA; 17 BP.  
 XX  
 AC ACN73120;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human GDMPLP-1 probe SEQ ID NO:10022.

XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX  
 OS Homo sapiens.

XX US2004137589-A1.  
 XX  
 PD 15-JUL-2004.

XX 26-NOV-2003; 2003US-00723361.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US0000661.  
 PR 30-JAN-2001; 2001WO-US0000662.  
 PR 30-JAN-2001; 2001WO-US0000663.  
 PR 30-JAN-2001; 2001WO-US0000664.  
 PR 30-JAN-2001; 2001WO-US0000665.  
 PR 30-JAN-2001; 2001WO-US0000666.  
 PR 30-JAN-2001; 2001WO-US0000667.  
 PR 30-JAN-2001; 2001WO-US0000668.  
 PR 30-JAN-2001; 2001WO-US0000669.  
 PR 30-JAN-2001; 2001WO-US0000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 PR 25-MAY-2001; 2001US-00866108.

XX (GUYY/) GU Y.  
 PA (JIYY/) JI Y.  
 PA (FENN/) PENN S G.  
 PA (HANZ/) HANZEL D K.

PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.  
 XX (SHAN/) SHANNON M R.  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 XX WPI; 2004-533376/51.  
 DR  
 XX Novel myosin-like protein-1, useful for treating or preventing disorder  
 PT associated with decreased expression or activity of human genome-derived  
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 PT function.  
 XX  
 PS Disclosure; SEQ ID NO 10022; Opp; English.  
 XX  
 CC The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (SI) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (SI), 95% deviation from (SI) which are conservative substitutions, and  
 CC 65% identity to (SI). A polypeptide of the invention acts as a agonist or  
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 15.6%; Score 12; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 98;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCCTC 38  
 Db 6 TCTGGAGTCCTC 17

RESULT 103  
 AAH18889  
 ID AAH18889 standard; DNA; 15 BP.

XX AAH18889;  
 AC AAH18889;

XX 21-JUN-2001 (first entry)

DE UCP3 polymorphism detection allele specific primer #2.

XX UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.

XX Homo sapiens.

XX WO200118232-A2.

XX 15-MAR-2001.

XX 08-SEP-2000; 2000WO-US024784.

XX 08-SEP-1999; 99US-0152789P.

XX (GENA-) GENAISANCE PHARM INC.  
 PA (STEP/) STEPHENS J C.

XX Chew A, Choi JY, Denton RR, Nandabalan K;

DR WPI; 2001-218562/22.

XX Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton  
 PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,  
 PT useful for the design of drugs for treating obesity.

XX Claim 15; Page 22; 94pp; English.

CC The present invention relates to the human uncoupling protein 3  
 CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The  
 CC polymorphisms are associated with obesity, especially diabetes mellitus  
 CC associated obesity. They polymorphisms may be identified and analysed to  
 CC determine whether an individual is susceptible to obesity and may be used  
 CC as the basis for targeted design of drugs to treat obesity. The present  
 CC sequence was used in the identification and amplification of UCP3  
 CC polymorphisms  
 CC  
 SQ Sequence 15 BP; 4 A; 5 C; 6 G; 0 T; 0 U; 0 Other;  
 Query Match 15.3%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 92;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCAGCG 58  
 DB 1 GGCACAGCCAGCG 15  
 ||| ||||| ||||| |||||

RESULT 104  
 AAF52028  
 ID AAF52028 standard; DNA; 15 BP.  
 XX  
 AC AAF52028;  
 DT 30-MAR-2001 (first entry)  
 XX  
 DE IGF-I oligonucleotide #2988.  
 XX  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200078341-A1.  
 XX  
 XX 28-DEC-2000.  
 XX  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX 21-JUN-1999; 99US-0140345P.  
 XX  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wright CJ, Werther GA, Edmondson SR;  
 XX  
 XX WPI; 2001-041421/05.  
 XX  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 8; Page 80; 201pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 CC  
 SQ Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 15.3%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 92;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 54 CAGCGAAGCTGATGT 68  
 DB 1 CAGCGCTGCTGATGT 15  
 ||||| ||||| ||||| |||||

RESULT 105  
 ABL53810  
 ID ABL53810 standard; DNA; 15 BP.  
 XX  
 AC ABL53810;  
 XX  
 DT 25-JUN-2002 (first entry)  
 XX  
 DE Equine infectious anemia virus DU gene coding sequence 3' fragment.  
 XX  
 KW EIAV; dUTPase; enzyme; DU gene; vaccine; infection; model; gene; ss.  
 XX  
 OS Equine infectious anemia virus.  
 XX  
 XX Key Location/Qualifiers  
 FH CDS 1..15  
 FT /tag= a  
 FT /product= "S2 peptide"  
 FT /note= "The CDS does not include a start or stop codon"  
 XX  
 PN WO200220051-A2.  
 XX  
 XX 14-MAR-2002.  
 XX  
 XX 06-SEP-2001; 2001WO-US027604.  
 XX  
 XX 09-SEP-2000; 2000US-00659030.  
 XX  
 XX (ALKU ) AKZO NOBEL NV.  
 XX  
 PI Montelaro RC, Puffer B, Li F, Issel C, Hennessey KJ, Brown KK;  
 XX  
 XX WPI; 2002-339776/37.  
 DR P-PSDB; ABB75741.  
 XX  
 XX Infecting equine with equine infectious anemia virus in order to  
 PT reproduce natural infection model which is useful for evaluating  
 PT immunogenicity of EIAV vaccine, involves administering a median horse  
 PT infective dose to equine.  
 XX  
 XX Example 1; Fig 5; 49pp; English.  
 PS  
 XX  
 CC The present sequence is a 3' fragment of the dUTPase (DU) gene coding  
 CC sequence of equine infectious anemia virus (EIAV). In the mutated  
 CC EIAVdeltaDU gene of the invention, this portion of the DU gene is ligated  
 CC to a 5' fragment (see ABL53809) of the gene, to produce a DU gene-deleted  
 CC construct (see ABL53811). The invention describes a vaccine for  
 CC effectively and safely immunising mammals, especially equids, from  
 CC disease caused by EIAV, the vaccine being tested for efficacy or  
 CC immunogenicity using an EIA challenge model of the invention. The  
 CC vaccine is a gene-deleted EIAV, e.g. a DU gene-deleted EIAV, which lacks  
 CC the ability to express the mutated gene protein in vivo, this lack of  
 CC expression being useful to differentiate vaccinated from non-vaccinated  
 CC or infected mammals. The multiple low dose EIA challenge model of the  
 CC invention can be used to determine the efficacy of vaccines, treatments  
 CC and diagnostic tests  
 XX



SQ Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 15.3%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 92;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCTGGGAT 21  
 ||||| ||||| |||||  
 Db 1 AGACAGCCTTGGGAT 15

RESULT 106  
 AAS19731  
 ID AAS19731 standard; DNA; 15 BP.  
 XX AC  
 XX AAS19731;  
 XX AC  
 XX AC  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE ASO probe #28 to detect human RANGAP1 gene polymorphisms.  
 XX  
 XX Human; single nucleotide polymorphism; SNP; RANGAP1;  
 KW haplotyping chromosome 22q13.2-q13.31; Ran GTPase activating protein 1;  
 KW genotyping; cancer; irregular cell cycle associated disorder; ASO; probe;  
 KW ss; allele-specific oligonucleotide.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200179240-A2.  
 XX PD 25-OCT-2001.  
 XX PF 17-APR-2001; 2001WO-US012455.  
 XX PR 17-APR-2000; 2000US-0198072P.  
 XX PA (GENA-) GENAISSANCE PHARM INC.  
 XX PI Chew A, Choi JY, Koehy B;  
 XX WPI; 2002-075068/10.  
 XX DR  
 XX  
 XX Genotyping human Ran GTPase activating protein 1 gene of individual for  
 PT determining haplotype of individual, involves determining identity of  
 PT nucleotide pair at specific polymorphic sites for two copies of the gene.  
 XX  
 PS Claim 15; Page 14; 148pp; English.  
 XX  
 CC The present invention relates to novel single nucleotide polymorphisms  
 CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene  
 CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or  
 CC genotyping the RANGAP1 gene. The methods of the invention make use of  
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or  
 CC primer-extension oligonucleotides for detecting the RANGAP1 gene  
 CC polymorphisms. The polynucleotides and screened compounds are useful for  
 CC treatment of diseases associated with RANGAP1 activity, such as cancer  
 CC and other disorders associated with an irregular cell cycle. AAS19704-  
 CC AAS19742 represent ASO probes for detecting human RANGAP1 gene  
 CC polymorphisms  
 XX  
 SQ Sequence 15 BP; 2 A; 4 C; 4 G; 4 T; 0 U; 1 Other;  
 Query Match 15.3%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 92;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTG 72  
 ||||| ||||| |||||  
 Db 1 GAACCTGTGCTCTG 15

RESULT 107  
 ABL53795

ID ABL53795 standard; DNA; 15 BP.  
 XX AC  
 XX ABL53795;  
 DT 25-JUN-2002 (first entry)  
 XX  
 DE Equine infectious anemia virus DU gene 3' fragment.  
 XX  
 XX EIAV; dUTPase; enzyme; DU gene; vaccine; diagnosis; gene; ss.  
 KW  
 XX Equine infectious anemia virus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 1..15  
 FT /\*tag= a  
 FT /product= "S2 peptide"  
 FT /partial  
 FT /note= "the CDS does not include a start or stop codon"  
 XX  
 XX WO200220041-A2.  
 XX PD 14-MAR-2002.  
 XX PF 06-SEP-2001; 2001WO-US027601.  
 XX PR 09-SEP-2000; 2000US-00658547.  
 XX PA (ALKU ) AKZO NOBEL NV.  
 XX PI Montaloro RC, Puffer B, Li P, Issel C, Hennessey KJ, Brown KK;  
 XX WPI; 2002-339773/37.  
 XX DR P-PSDB; ABB75736.  
 XX PT Novel vaccine comprising gene-mutated equine infectious anemia virus  
 PT which lacks ability to express mutated gene protein in vivo, useful for  
 PT immunizing horses against disease caused by equine infectious anemia  
 PT virus.  
 XX  
 XX Example 6; Fig 5; 54pp; English.  
 XX  
 CC The present sequence is a 3' fragment of the dUTPase (DU) gene coding  
 CC sequence of equine infectious anemia virus (EIAV). In the mutated  
 CC EIAVdeltaDU gene of the invention, this portion of the DU gene is ligated  
 CC to a 5' fragment (see ABL53794) of the gene, to generate the sequence  
 CC given in ABL53796. Two StyI sites flanking the gene are used to create  
 CC the deletion, removing 80% of the DU coding sequence, including 4 of 5  
 CC conserved amino acid motifs. The invention relates to EIA vaccines that  
 CC provide immunity to mammals, especially to equines, from infection with  
 CC EIAV, and which allow differentiation between vaccinated and non-  
 CC vaccinated, but exposed, animals. The vaccine has at least 1 mutation in  
 CC the EIAV, e.g. the present DU gene-mutated EIAV construct, which produces  
 CC a non-functional gene in the vaccine virus. Deletion of the DU gene does  
 CC not reduce the ability of the mutated EIAV to replicate in cell culture,  
 CC allowing large-scale vaccine production. The vaccine cannot cause  
 CC clinical disease or spread to other animals. The mutated region can also  
 CC be used as an insertion point for foreign genes, using EIAV as a vector  
 CC for vaccination against diseases other than EIA  
 XX  
 SQ Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 15.3%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 92;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCTGGGAT 21  
 ||||| ||||| |||||  
 Db 1 AGACAGCCTTGGGAT 15

RESULT 108  
 ACF57576  
 ID ACF57576 standard; DNA; 15 BP.

```

XX ACFS57576;
XX
XX 22-APR-2004 (first entry)
XX
XX Human ALDOB gene allele-specific primer SEQ ID NO: 27.
XX
XX Human; ALDOB; fructose-bisphosphate aldolase B; SNP;
XX single nucleotide polymorphism; primer; probe; ss.
XX
XX Homo sapiens.
XX
XX WC2003091454-A1.
XX
XX 06-NOV-2003.
XX
XX 26-APR-2002; 2002WO-US013328.
XX
XX 26-APR-2002; 2002WO-US013328.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Chew A, Kazemi A, Koshy B;
XX
XX WPI; 2003-877338/81.
XX
XX Claim 39; Page 14; Opp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX fructose-bisphosphate aldolase B (ALDOB) and single nucleotide
XX polymorphisms (SNPs) which have been identified in each sequence. The
XX method of haplotyping the sequences is useful for haplotyping the
XX fructose-bisphosphate aldolase B (ALDOB) gene of an individual or for
XX validating the ALDOB protein as a candidate target for treating a medical
XX condition predicted to be associated with ALDOB activity. The present
XX sequence is an allele-specific primer/probe used to identify the
XX haplotype of the human ALDOB gene in the exemplification of the invention
XX
XX Sequence 15 BP; 6 A; 2 C; 5 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 15.3%; Score 11.8; DB 1; Length 15;
XX Best Local Similarity 86.7%; Pred. No. 92;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 41 AGAGGTAAAGAGCCA 55
DB 1 AGAGGTCAAGAGCRA 15
||||| |||||

RESULT 109
ADJ82347
ID ADJ82347 standard; DNA; 15 BP.
XX
XX ADJ82347;
XX
XX 06-MAY-2004 (first entry)
XX
XX KLM5Y-encoding nucleotide #75.
XX
XX ss; cytosstatic; platelet-derived growth factor receptor; PDGF-R; cancer;
XX carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
XX neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
XX myeloproliferative disease; blood vessel proliferative disease;
XX angiogenesis.
XX
XX Synthetic.
XX
XX WO2003045973-A2.
XX
XX 05-JUN-2003.
XX
XX 30-SEP-2002; 2002WO-US031165.
XX
XX Dean C, Heidaran M, Spargo CA;

PR 28-NOV-2001; 2001US-0333476P.
XX
XX (BECT ) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX
XX Dean C, Heidaran M, Spargo CA;
XX
XX WPI; 2003-505179/47.
XX
XX New peptides having growth inhibitory action, useful for inhibiting tumor
XX or cancer cell proliferation, or for treating fibrotic disorders,
XX myeloproliferative diseases, and blood vessel proliferative (angiogenic)
XX disorders.
XX
XX Disclosure; SEQ ID NO 128; 48pp; English.
XX
XX The invention relates to an isolated peptide or polypeptide (I) of no
XX more than about 50 amino acid residues which when contacted with cells in
XX which a platelet-derived growth factor receptor (PDGF-R) is activated in
XX an autocrine manner, inhibits the growth of these cells. The isolated
XX peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
XX Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
XX Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell
XX proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
XX sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
XX or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
XX ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
XX muscle or bone cell. The peptides are also useful for treating fibrotic
XX disorders, myeloproliferative diseases, and blood vessel proliferative
XX (angiogenic) disorders. This sequence represents a possible nucleotide
XX encoding the P3 peptide.
XX
XX Sequence 15 BP; 4 A; 3 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 15.3%; Score 11.8; DB 1; Length 15;
XX Best Local Similarity 86.7%; Pred. No. 92;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AGCTGATGTCCTGT 73
DB 1 AGCTTATGTCCTAT 15
||||| |||||

RESULT 110
ADJ82397
ID ADJ82397 standard; DNA; 15 BP.
XX
XX ADJ82397;
XX
XX 06-MAY-2004 (first entry)
XX
XX KLM5Y-encoding nucleotide #125.
XX
XX ss; cytosstatic; platelet-derived growth factor receptor; PDGF-R; cancer;
XX carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
XX neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
XX myeloproliferative disease; blood vessel proliferative disease;
XX angiogenesis.
XX
XX Synthetic.
XX
XX WO2003045973-A2.
XX
XX 05-JUN-2003.
XX
XX 30-SEP-2002; 2002WO-US031165.
XX
XX 28-NOV-2001; 2001US-0333476P.
XX
XX (BECT ) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX
XX Dean C, Heidaran M, Spargo CA;

```

XX WPI; 2003-505179/47.

XX New peptides having growth inhibitory action, useful for inhibiting tumor

PT or cancer cell proliferation, or for treating fibrotic disorders,

PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)

PT disorders.

XX Disclosure; SEQ ID NO 178; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no

CC more than about 50 amino acid residues which when contacted with cells in

CC which a platelet-derived growth factor receptor (PDGFR) is activated in

CC an autocrine manner, inhibits the growth of these cells. The isolated

CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-

CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-

CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell

CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,

CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,

CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,

CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,

CC muscle or bone cell. The peptides are also useful for treating fibrotic

CC disorders, myeloproliferative diseases, and blood vessel proliferative

CC (angiogenic) disorders. This sequence represents a possible nucleotide

CC encoding the P3 peptide.

XX Sequence 15 BP; 5 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

SQ Query Match 15.3%; Score 11.8; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 92;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGT 73

|||||

Db 1 AAGCTGATGTCATAT 15

RESULT 111

ADJ82379

ID ADJ82379 standard; DNA; 15 BP.

XX AC ADJ82379;

XX 06-MAY-2004 (first entry)

DE KLMYS-encoding nucleotide #107.

XX ss; cytostatic; platelet-derived growth factor receptor; PDGFR; cancer;

KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;

KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;

KW myeloproliferative disease; blood vessel proliferative disease;

KW angiogenesis.

XX OS Synthetic.

XX W02003045973-A2.

XX 05-JUN-2003.

XX 30-SEP-2002; 2002WO-US031165.

XX 28-NOV-2001; 2001US-0333476P.

XX (BECT ) BECTON DICKINSON & CO.

PA (HAAL/) HAALAND P D.

XX Dean C, Heidaran M, Spargo CA;

XX WPI; 2003-505179/47.

XX New peptides having growth inhibitory action, useful for inhibiting tumor

PT or cancer cell proliferation, or for treating fibrotic disorders,

PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)

PT disorders.

XX Disclosure; SEQ ID NO 160; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no

CC more than about 50 amino acid residues which when contacted with cells in

CC which a platelet-derived growth factor receptor (PDGFR) is activated in

CC an autocrine manner, inhibits the growth of these cells. The isolated

CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-

CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-

CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell

CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,

CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,

CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,

CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,

CC muscle or bone cell. The peptides are also useful for treating fibrotic

CC disorders, myeloproliferative diseases, and blood vessel proliferative

CC (angiogenic) disorders. This sequence represents a possible nucleotide

CC encoding the P3 peptide.

XX Sequence 15 BP; 5 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

SQ Query Match 15.3%; Score 11.8; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 92;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGT 73

|||||

Db 1 AAGCTAATGTCCTAT 15

RESULT 112

ADJ82331

ID ADJ82331 standard; DNA; 15 BP.

XX AC ADJ82331;

XX 06-MAY-2004 (first entry)

DE KLMYS-encoding nucleotide #59.

XX ss; cytostatic; platelet-derived growth factor receptor; PDGFR; cancer;

KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;

KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;

KW myeloproliferative disease; blood vessel proliferative disease;

KW angiogenesis.

XX OS Synthetic.

XX W02003045973-A2.

XX 05-JUN-2003.

XX 30-SEP-2002; 2002WO-US031165.

XX 28-NOV-2001; 2001US-0333476P.

XX (BECT ) BECTON DICKINSON & CO.

PA (HAAL/) HAALAND P D.

XX Dean C, Heidaran M, Spargo CA;

XX WPI; 2003-505179/47.

XX New peptides having growth inhibitory action, useful for inhibiting tumor

PT or cancer cell proliferation, or for treating fibrotic disorders,

PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)

PT disorders.

XX Disclosure; SEQ ID NO 112; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no

CC more than about 50 amino acid residues which when contacted with cells in

CC which a platelet-derived growth factor receptor (PDGF-R) is activated in  
 CC an autocrine manner, inhibits the growth of these cells. The isolated  
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-  
 CC Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-  
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (1) is useful for inhibiting cell  
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,  
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,  
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,  
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,  
 CC muscle or bone cell. The peptides are also useful for treating fibrotic  
 CC disorders, myeloproliferative diseases, and blood vessel proliferative  
 CC (angiogenic) disorders. This sequence represents a possible nucleotide  
 CC encoding the P3 peptide.

XX  
 SQ Sequence 15 BP; 5 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 15.3%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 92;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGT 73  
 DB 1 AAATGATGTCCTAT 15

RESULT 113  
 ADJ82363  
 ID ADJ82363 standard; DNA; 15 BP.  
 AC  
 AC ADJ82363;  
 XX  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE KLMSY-encoding nucleotide #91.  
 XX  
 XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;  
 KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;  
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;  
 KW myeloproliferative disease; blood vessel proliferative disease;  
 KW angiogenesis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2003045973-A2.  
 PN  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 30-SEP-2002; 2002WO-US031165.  
 XX  
 XX 28-NOV-2001; 2001US-0333476P.  
 PR  
 XX (BECT ) BECTON DICKINSON & CO.  
 PA (HAAL/) HAALAND P D.  
 XX  
 PI Dean C, Heidaran M, Spargo CA;  
 XX  
 XX WPI; 2003-505179/47.  
 DR  
 XX New peptides having growth inhibitory action, useful for inhibiting tumor  
 PT or cancer cell proliferation, or for treating fibrotic disorders,  
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)  
 PT disorders.  
 XX  
 PS Disclosure; SEQ ID NO 144; 48pp; English.  
 XX  
 CC The invention relates to an isolated peptide or polypeptide (1) of no  
 CC more than about 50 amino acid residues which when contacted with cells in  
 CC which a platelet-derived growth factor receptor (PDGF-R) is activated in  
 CC an autocrine manner, inhibits the growth of these cells. The isolated  
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-  
 CC Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-  
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (1) is useful for inhibiting cell  
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,  
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,  
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,  
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,  
 CC muscle or bone cell. The peptides are also useful for treating fibrotic  
 CC disorders, myeloproliferative diseases, and blood vessel proliferative  
 CC (angiogenic) disorders. This sequence represents a possible nucleotide  
 CC encoding the P3 peptide.

CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,  
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,  
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,  
 CC muscle or bone cell. The peptides are also useful for treating fibrotic  
 CC disorders, myeloproliferative diseases, and blood vessel proliferative  
 CC (angiogenic) disorders. This sequence represents a possible nucleotide  
 CC encoding the P3 peptide.

XX  
 SQ Sequence 15 BP; 4 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 15.3%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 92;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGT 73  
 DB 1 AAGCTGATGTCCTAT 15

RESULT 114  
 ADJ82387  
 ID ADJ82387 standard; DNA; 15 BP.  
 XX  
 AC  
 AC ADJ82387;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE KLMSY-encoding nucleotide #115.  
 XX  
 KW ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;  
 KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;  
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;  
 KW myeloproliferative disease; blood vessel proliferative disease;  
 KW angiogenesis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2003045973-A2.  
 PN  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 30-SEP-2002; 2002WO-US031165.  
 XX  
 XX 28-NOV-2001; 2001US-0333476P.  
 PR  
 XX (BECT ) BECTON DICKINSON & CO.  
 PA (HAAL/) HAALAND P D.  
 XX  
 PI Dean C, Heidaran M, Spargo CA;  
 XX  
 XX WPI; 2003-505179/47.  
 DR  
 XX New peptides having growth inhibitory action, useful for inhibiting tumor  
 PT or cancer cell proliferation, or for treating fibrotic disorders,  
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)  
 PT disorders.  
 XX  
 PS Disclosure; SEQ ID NO 168; 48pp; English.  
 XX  
 CC The invention relates to an isolated peptide or polypeptide (1) of no  
 CC more than about 50 amino acid residues which when contacted with cells in  
 CC which a platelet-derived growth factor receptor (PDGF-R) is activated in  
 CC an autocrine manner, inhibits the growth of these cells. The isolated  
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-  
 CC Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-  
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (1) is useful for inhibiting cell  
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,  
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,  
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,  
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,  
 CC muscle or bone cell. The peptides are also useful for treating fibrotic  
 CC disorders, myeloproliferative diseases, and blood vessel proliferative  
 CC (angiogenic) disorders. This sequence represents a possible nucleotide  
 CC encoding the P3 peptide.

CC encoding the P3 peptide.  
 SQ Sequence 15 BP; 5 A; 3 C; 2 G; 5 T; 0 U; 0 Other;  
 Query Match 15.3%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 92;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGT 73  
 DB 1 AAGCTGATGTCCTAT 15

RESULT 116  
 ADJ82393  
 ID ADJ82393 standard; DNA; 15 BP.  
 XX  
 AC ADJ82393;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE KLMYSY-encoding nucleotide #121.  
 XX  
 KW ss; cytotostatic; platelet-derived growth factor receptor; PDGF-R; cancer;  
 KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;  
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;  
 KW myeloproliferative disease; blood vessel proliferative disease;  
 KW angiogenesis.  
 XX  
 OS Synthetic.  
 XX  
 PN W02003045973-A2.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 30-SEP-2002; 2002WO-US031165.  
 XX  
 PR 28-NOV-2001; 2001US-0333476P.  
 XX  
 PA (BECT ) BECTON DICKINSON & CO.  
 PA (HAAL/) HAALAND P D.  
 XX  
 PI Dean C, Heidaran M, Spargo CA;  
 XX  
 DR WPI; 2003-505179/47.  
 XX  
 PT New peptides having growth inhibitory action, useful for inhibiting tumor  
 PT or cancer cell proliferation, or for treating fibrotic disorders,  
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)  
 PT disorders.  
 XX  
 PS Disclosure; SEQ ID NO 174; 48pp; English.  
 XX  
 CC The invention relates to an isolated peptide or polypeptide (I) of no  
 CC more than about 50 amino acid residues which when contacted with cells in  
 CC which a platelet-derived growth factor receptor (PDGF-R) is activated in  
 CC an autocrine manner, inhibits the growth of these cells. The isolated  
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-  
 CC Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-  
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell  
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,  
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,  
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,  
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,  
 CC muscle or bone cell. The peptides are also useful for treating fibrotic  
 CC disorders, myeloproliferative diseases, and blood vessel proliferative  
 CC (angiogenic) disorders. This sequence represents a possible nucleotide  
 CC encoding the P3 peptide.  
 XX  
 SQ Sequence 15 BP; 4 A; 2 C; 3 G; 6 T; 0 U; 0 Other;

-Query Match 15.3%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 92;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGT 73  
 DB 1 AAGCTGATGTCCTAT 15

RESULT 115  
 ADJ82399  
 ID ADJ82399 standard; DNA; 15 BP.  
 XX  
 AC ADJ82399;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE KLMYSY-encoding nucleotide #127.  
 XX  
 KW ss; cytotostatic; platelet-derived growth factor receptor; PDGF-R; cancer;  
 KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;  
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;  
 KW myeloproliferative disease; blood vessel proliferative disease;  
 KW angiogenesis.  
 XX  
 OS Synthetic.  
 XX  
 PN W02003045973-A2.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 30-SEP-2002; 2002WO-US031165.  
 XX  
 PR 28-NOV-2001; 2001US-0333476P.  
 XX  
 PA (BECT ) BECTON DICKINSON & CO.  
 PA (HAAL/) HAALAND P D.  
 XX  
 PI Dean C, Heidaran M, Spargo CA;  
 XX  
 DR WPI; 2003-505179/47.  
 XX  
 PT New peptides having growth inhibitory action, useful for inhibiting tumor  
 PT or cancer cell proliferation, or for treating fibrotic disorders,  
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)  
 PT disorders.  
 XX  
 PS Disclosure; SEQ ID NO 180; 48pp; English.  
 XX  
 CC The invention relates to an isolated peptide or polypeptide (I) of no  
 CC more than about 50 amino acid residues which when contacted with cells in  
 CC which a platelet-derived growth factor receptor (PDGF-R) is activated in  
 CC an autocrine manner, inhibits the growth of these cells. The isolated  
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-  
 CC Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-  
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell  
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,  
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,  
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,  
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,  
 CC muscle or bone cell. The peptides are also useful for treating fibrotic  
 CC disorders, myeloproliferative diseases, and blood vessel proliferative  
 CC (angiogenic) disorders. This sequence represents a possible nucleotide  
 CC encoding the P3 peptide.  
 XX  
 SQ Sequence 15 BP; 4 A; 2 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 15.3%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 92;

RESULT 117  
ADT41519  
ID ADT41519 standard; DNA; 15 BP.  
XX AC  
XX ADT41519;  
XX DT 27-JAN-2005 (first entry)  
XX DE EIAV dUTPase (DU) C-terminal DNA.  
XX EIAV; S2 protein; vaccine; envelope protein; Tat protein;  
KW lentiviral disease; EIAV infection; ds; dUTPase; DU.  
XX OS Equine infectious anemia virus.  
XX US2004219166-A1.  
XX PD 04-NOV-2004.  
XX PF 24-JUL-2003; 2003US-00627568.  
XX PR 09-SEP-2000; 2000US-00658547.  
XX PR 26-JUN-2002; 2002US-00180626.  
XX (MONT/) MONTELABO R C.  
PA (CRAI/) CRAIGO J.  
PA (LIFF/) LI F.  
XX Montelaro RC, Craigo J, Li F;  
PI WPI; 2004-774916/76.  
XX P-PSDB; ADT41520.  
XX New construct comprising gene-mutated equine infectious anemia virus  
PT (EIAV) for providing immunity from diseases caused by EIAV and allowing  
PT diagnostic differentiation between vaccinated and non-vaccinated mammals  
PT (i.e. horses).  
XX Example 6; Fig 5; 3lpp; English.  
XX The invention relates to a construct comprising a gene-mutated equine  
XX infectious anemia virus (EIAV) comprising two redundant stop codons and a  
CC deletion (in the S2 protein) where the virus lacks the ability to express  
CC the mutated gene protein in vivo and where the lack of expression can be  
CC used to differentiate vaccinated from non-vaccinated or infected mammals.  
CC Also included are a diagnostic test for differentiating mammals  
CC vaccinated with the above construct from non-vaccinated mammals/infected  
CC mammals (comprising one or more reagents for demonstrating the absence  
CC of a normal EIAV gene expression product or a normal gene sequence in  
CC mammals vaccinated with the gene-mutated construct and a measurable level  
CC of the expression product or amount of the normal gene sequence in  
CC infected mammals) and a method of differentiating a vaccinated mammal  
CC from a non-vaccinated mammal (comprising obtaining a sample from a test  
CC mammal, and analysing the sample for the presence of a gene expression  
CC product normally produced by wild-type EIAV but not produced by the EIAV  
CC construct cited above). The two redundant stop codons are inserted into  
CC the S2 open reading frame at positions corresponding to amino acids Gly5  
CC and Gly18. The stop codon does not affect normal expression of the  
CC envelope protein. The deletion is a deletion of about 6-25 base pairs and  
CC is located at least 7 base pairs downstream of the stop codon of the  
CC second coding region of Tat. The deletion does not interrupt the splice  
CC donor 2 site downstream of the stop codon of the second coding region of  
CC Tat and upstream of the initiation codon of the S2 open reading frame.  
CC The generation of the stop codon at Gly5 further comprises the insertion  
CC of a restriction endonuclease site where the restriction endonuclease is  
CC a molecular marker for differentiating between wild type EIAV and the  
CC gene-mutated EIAV. The construct is useful for immunising mammals (e.g.  
CC horses) against lentiviral diseases, particularly EIAV infection. The  
CC construct and method may also be used for differentiating vaccinated  
CC mammals from non-vaccinated or infected mammals. Deletions were also  
CC contemplated in the DU (dUTPase) gene of EIAV. The present sequence is  
CC the wild-type EIAV DU 5' or 3' end.

XX SQ Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 15.3%; Score 11.8; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 92;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 7 AGACGGCCTGGGAT 21  
DB 1 AGACGGCCTGGGAT 15  
RESULT 118  
AAQ32194/c  
ID AAQ32194 standard; DNA; 16 BP.  
XX AC AAQ32194;  
XX AC  
XX DT 25-MAR-2003 (revised)  
XX DT 27-APR-1993 (first entry)  
XX DE Consensus 16n repeat of major IE gene promoter region.  
XX Human; cytomegalovirus; CMV; immediate-early; transcription; ss.  
XX Synthetic.  
XX US5168062-A.  
XX PD 01-DEC-1992.  
XX PF 10-SEP-1990; 90US-00582130.  
XX PR 30-JAN-1985; 85US-00696617.  
XX PR 22-MAY-1987; 87US-00058662.  
XX PR 05-OCT-1988; 88US-00256134.  
XX (IOWA ) UNIV IOWA STATE RES FOUND INC.  
XX Stinski MF;  
XX WPI; 1992-424148/51.  
XX Plasmids and DNA for transforming host cells - contain human  
PT cytomegalovirus immediate-early, promoter-regulatory DNA sequence.  
XX Claim 3; Fig 3; 5pp; English.  
XX The sequence represents a consensus 16 base pair repeat found in the  
CC human cytomegalovirus promoter regulatory region of the major immediate  
CC early gene, representing the nucleotides most frequently found within the  
CC 16n repeat. The promoter region contains the typical TATA and CAAT boxes  
CC and three different sets of repeat sequences, designated 19n, 18n and 16n  
CC repeats. Each repeat sequence is repeated at least 4 times. There is a  
CC 21n repeat sequence which is repeated twice. The repeat sequence and/or  
CC the surrounding sequences play a critical role in the relative level of  
CC expression of the downstream gene. Experiments using various deletions of  
CC the regulatory sequence suggest a direct correlation between the number  
CC of repeats and the relative level of gene expression. Hence these  
CC sequences or adjacent sequences constitute a component of the regulatory  
CC region that enhances the level of expression of the adjacent gene. These  
CC components are referred to as enhancers or activators. See also AAQ32183-  
CC 95 and AAQ32430-4. (Updated on 25-MAR-2003 to correct PF field.)  
XX SQ Sequence 16 BP; 5 A; 4 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 15.3%; Score 11.8; DB 1; Length 16;  
Best Local Similarity 86.7%; Pred. No. 98;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 63 TGATGTCCTGTCAAG 77  
DB 15 TGATGTCCTGTCAAG 1

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RESULT 119
AAQ32195/c
ID AAQ32195 standard; DNA; 16 BP.
XX
XX
AC AAQ32195;
XX
XX 25-MAR-2003 (revised)
DT 27-APR-1993 (first entry)
XX
XX 16n repeat of major IE gene promoter region.
XX
XX Human; cytomegalovirus; CMV; immediate-early; transcription; ss.
XX
XX Synthetic.
XX
XX US5168062-A.
XX
XX 01-DEC-1992.
XX
XX 10-SEP-1990; 90US-00582130.
XX
XX 30-JAN-1985; 85US-00696617.
XX
XX 22-MAY-1987; 87US-00058662.
XX
XX 05-OCT-1988; 88US-00256134.
XX
XX (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX Stinski MF;
XX
XX WPI; 1992-424148/51.
XX
XX Plasmids and DNA for transforming host cells - contain human
XX cytomegalovirus immediate-early, promoter-regulatory DNA sequence.
XX
XX Claim 3; Fig 3; 5pp; English.
XX
XX The sequence represents a 16 base pair repeat found in the human
XX cytomegalovirus promoter regulatory region of the major immediate early
XX gene from nucleotides -371 to -356 (distance from the cap site). The
XX promoter region contains the typical TATA and CAAT boxes and three
XX different sets of repeat sequences, designated 19n, 18n and 16n repeats.
XX Each repeat sequence is repeated at least 4 times. There is a 21n repeat
XX sequence which is repeated twice. The repeat sequence and/or the
XX surrounding sequences play a critical role in the relative level of
XX expression of the downstream gene. Experiments using various deletions of
XX the regulatory sequence suggest a direct correlation between the number
XX of repeats and the relative level of gene expression. Hence these
XX sequences or adjacent sequences constitute a component of the regulatory
XX region that enhances the level of expression of the adjacent gene. These
XX components are referred to as enhancers or activators. See also AAQ32183-
XX 94 and AAQ32430-4. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 16 BP; 5 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 15.3%; Score 11.8; DB 1; Length 16;
XX Best Local Similarity 86.7%; Pred. No. 98;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 63 TGATGTCCTGTCAAG 77
XX 15 TGATGTACTGCCAAG 1
XX
XX RESULT 120
AAQ81491/c
ID AAQ81491 standard; DNA; 16 BP.
XX
XX AC AAQ81491;
XX
XX 25-MAR-2003 (revised)
DT 29-AUG-1995 (first entry)
XX
XX CMV; HCMV; major immediate-early; IE gene; IEPR; vector; transcription;
XX gene expression; pIEPR12; ss.
XX
XX Human cytomegalovirus.
XX
XX US5385839-A.
XX
XX 31-JAN-1995.
XX
XX 17-JUN-1992; 92US-00900056.
XX
XX 30-JAN-1985; 85US-00696617.
XX
XX 22-MAY-1987; 87US-00058662.
XX
XX 05-OCT-1988; 88US-00256134.
XX
XX 10-SEP-1990; 90US-00582130.
XX
XX (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX Stinski MF;
XX
XX WPI; 1995-081566/11.
XX
XX New transfer vectors for gene expression - comprising the immediate-early
XX promoter regulatory region of human cytomegalovirus.
XX
XX Disclosure; Fig 3; 10pp; English.
XX
XX The HCMV immediate-early promoter regulatory (IEPR) region, shown in
XX AAQ81478, enhances the transcription and expression of adjacent genes in
XX human cells, and has been used to construct gene transfer vector pIEPR12
XX (NRRL B-15930). The IEPR region includes 19n, 18n and 16n repeat sets,
XX each repeated 4 times, and a 21n set repeated twice. The 16n set is given
XX in AAQ81491-94, with the consensus in AAQ81490. (Updated on 25-MAR-2003
XX to correct PF field.)
XX
XX Sequence 16 BP; 5 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 15.3%; Score 11.8; DB 1; Length 16;
XX Best Local Similarity 86.7%; Pred. No. 98;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 63 TGATGTCCTGTCAAG 77
XX 15 TGATGTACTGCCAAG 1
XX
XX RESULT 121
AAQ81490/c
ID AAQ81490 standard; DNA; 16 BP.
XX
XX AC AAQ81490;
XX
XX 25-MAR-2003 (revised)
DT 29-AUG-1995 (first entry)
XX
XX IEPR 16n repeat consensus.
XX
XX CMV; HCMV; major immediate-early; IE gene; IEPR; vector; transcription;
XX gene expression; pIEPR12; ss.
XX
XX Human cytomegalovirus.
XX
XX US5385839-A.
XX
XX 31-JAN-1995.
XX
XX 17-JUN-1992; 92US-00900056.
XX
XX 30-JAN-1985; 85US-00696617.
XX
XX 22-MAY-1987; 87US-00058662.

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PR 05-OCT-1988; 88US-00256134.
PR 10-SEP-1990; 90US-00582130.
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX Stinski MF;
PI
XX
XX WPI; 1995-081566/11.
XX
XX New transfer vectors for gene expression - comprising the immediate-early
PT promoter regulatory region of human cytomegalovirus.
XX
XX Disclosure; Fig 3; 10pp; English.
XX
XX The HCMV immediate-early promoter regulatory (IEPR) region, shown in
CC AAQ81478, enhances the transcription and expression of adjacent genes in
CC human cells, and has been used to construct gene transfer vector pIEPR12
CC (NRRL B-15930). The IEPR region includes 19n, 18n and 16n repeat sets,
CC each repeated 4 times, and a 21n set repeated twice. The 16n set is given
CC in AAQ81491-94, with the consensus in AAQ81490. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
XX Sequence 16 BP; 5 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
SQ
    Query Match      15.3%; Score 11.8; DB 1; Length 16;
    Best Local Similarity 86.7%; Pred. No. 98;
    Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 63 TGATGTCCTGTCAAG 77
Db 15 TGATGTACTGCCAAG 1

RESULT 122
AAV26760/c
ID AAV26760 standard; DNA; 16 BP.
XX
XX AAV26760;
AC
XX
XX 24-SEP-1998 (first entry)
DE Human cytomegalovirus immediate-early promoter fusion site 16.
XX
XX ss; gag; gene delivery; pol; env; murine leukaemia virus; gene therapy.
XX
XX Synthetic.
OS
XX
XX WO9812338-A1.
PN
XX
XX 26-MAR-1998.
PD
XX
XX 22-SEP-1997; 97WO-KR000180.
PF
XX
XX 21-SEP-1996; 96KR-00041438.
PR
XX
XX (VIRO-) VIROMEDICA PACIFIC LTD.
PA
XX
XX Kim S, Kim S, Robbins PD;
PI
XX
XX WPI; 1998-217273/19.
DR
XX
XX New retroviral vectors, particularly for gene therapy - which are free of
PT the gag coding sequence, to provide for high levels of gene expression,
PT viral titre and packaging efficiency.
XX
XX Disclosure; Fig 7; 79pp; English.
PS
XX
XX The fusion sites AAV26756-V26760 were used in the production of two
CC retroviral vectors (RV). The first is a RV that has no gag coding
CC sequence is capable of delivering a gene of interest to a target cell
CC when packaging functions of gag, pol and env are provided. The second is
CC a RV based on murine leukaemia virus (MLV) where entire gag and env
CC coding sequences are completely deleted. The vectors can be used for gene

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CC therapy, for example for the delivery of hormones, enzymes, receptors or
CC drugs
XX
XX Sequence 16 BP; 5 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
SQ
    Query Match      15.3%; Score 11.8; DB 1; Length 16;
    Best Local Similarity 86.7%; Pred. No. 98;
    Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 63 TGATGTCCTGTCAAG 77
Db 15 TGATGTACTGCCAAG 1

RESULT 123
ABK72351/c
ID ABK72351 standard; DNA; 15 BP.
XX
XX ABK72351;
AC
XX
XX 30-JUL-2002 (first entry)
DT
XX
XX Human HTR5A gene allele-specific oligonucleotide probe #13.
DE
XX
XX Human; 5-hydroxytryptamine receptor 5A; HTR5A; serotonin; probe; ss;
KW neuroprotective; neurological disease; depression; epilepsy;
KW gene therapy; single nucleotide polymorphism; haplotype pair;
KW chromosome 7q36.1.
XX
XX Homo sapiens.
OS
XX
XX WO200222887-A1.
PN
XX
XX 21-MAR-2002.
PD
XX
XX 17-SEP-2001; 2001WO-US029210.
PF
XX
XX 15-SEP-2000; 2000US-0233051P.
PR
XX
XX (GENA-) GENAISANCE PHARM INC.
PA
XX
XX Kazemi A, Koshiy B, Sanchis A, Tirrell C;
PI
XX
XX WPI; 2002-393978/42.
DR
XX
XX Novel genetic variants of 5-Hydroxytryptamine (Serotonin) Receptor 5A
PT isogenes, useful for improving efficiency and reliability in drug
PT development for treating neurological diseases.
XX
XX Claim 17; Page 14; 134pp; English.
PS
XX
XX The invention relates to single nucleotide polymorphisms in the gene
CC encoding human 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A). A
CC method for haplotyping the HTR5A gene in an individual comprises
CC identifying the nucleotide at one or more polymorphic sites and
CC determining whether one of the copies of the gene is defined by one of
CC the HTR5A haplotypes given in the specification or whether both copies
CC are defined by a haplotype pair. This method is useful in genotyping,
CC whereby all possible haplotype pairs can be assigned to specific
CC genotypes. An association between a trait and a haplotype or haplotype
CC pair of the HTR5A gene can be identified by comparing the frequency of
CC the haplotype or haplotype pair in a population exhibiting the trait with
CC the frequency of the haplotype or haplotype pair in a reference
CC population, where a higher haplotype frequency in the trait population
CC indicates the trait is associated with the haplotype or haplotype pair.
CC HTR5A and its corresponding DNA are used for studying the expression and
CC function of HTR5A, and in screening for candidate drugs to treat diseases
CC related to HTR5A activity, such as neurological disorders, including
CC depression and epilepsy. Sequences ABK72339-ABK72358 represent allele-
CC specific oligonucleotide probes used for detecting HTR5A gene
CC polymorphisms
XX
XX Sequence 15 BP; 2 A; 8 C; 2 G; 2 T; 0 U; 1 Other;
SQ

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Query Match      15.1%; Score 11.6; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. NO. 98;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGCTGGGGGATA 22
Db 12 GGCCGGGGGATA 1

RESULT 124
ABF84445/c
ID ABF844445 standard; DNA; 13 BP.
XX AC ABF844445;
XX XX
DT 22-FEB-2002 (first entry)
XX XX
DE Oligonucleotide SEQ ID NO 184442 for detecting SNP TSC0045516.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
FN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT
XX XX
DE Oligonucleotide SEQ ID NO 184442 for detecting SNP TSC0045516.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
FN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT
XX XX
DE Oligonucleotide SEQ ID NO 184442; 29pp + Sequence Listing; German.
XX XX
PR 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 184442; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. NO. 90;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGCTAAGA 51
Db 13 TGAGATGTAAGA 1

RESULT 125
ABC41770
ID ABC41770 standard; DNA; 13 BP.

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XX AC ABC41770;
XX XX
DT 21-FEB-2002 (first entry)
XX XX
DE Oligonucleotide SEQ ID NO 41787 for detecting SNP TSC0012525.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
FN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT
XX XX
DE Oligonucleotide SEQ ID NO 41787; 29pp + Sequence Listing; German.
XX XX
PR 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 41787; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. NO. 90;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGCTAAGA 51
Db 1 TGAGAGGCTAAGA 13

RESULT 126
ABF84444
ID ABF844444 standard; DNA; 13 BP.
XX AC ABF844444;
XX XX
DT 22-FEB-2002 (first entry)
XX XX
DE Oligonucleotide SEQ ID NO 184441 for detecting SNP TSC0045516.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX

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SQ Sequence 14 BP; 2 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 14;  
 Best Local Similarity 92.3%; Pred. No. 98;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 60 AGCTGATGCTCTGG 72  
 Db 2 AGCTGATGCCCTG 14  
 |||||

RESULT 129  
 AAF48760  
 ID AAF48760 standard; DNA; 15 BP.  
 XX  
 AC AAF48760;  
 XX  
 DT 30-MAR-2001 (first entry)  
 XX  
 DE IGFBP3 oligonucleotide #2180.  
 XX  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wraight CJ, Werther GA, Edmondson SR;  
 XX  
 DR WPI; 2001-041421/05.  
 XX  
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 7; Page 58; 201pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 92.3%; Pred. No. 1.1e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 GATACAACTCTGG 31  
 Db 1 GATACAACTCTGG 13  
 |||||

RESULT 130  
 AAF48758  
 ID AAF48758 standard; DNA; 15 BP.  
 XX  
 AC AAF48758;  
 XX  
 DT 30-MAR-2001 (first entry)  
 XX  
 DE IGFBP3 oligonucleotide #2178.  
 XX  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wraight CJ, Werther GA, Edmondson SR;  
 XX  
 DR WPI; 2001-041421/05.  
 XX  
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 7; Page 58; 201pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 5 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 92.3%; Pred. No. 1.1e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 GATACAACTCTGG 31  
 |||||

```

Db          3  GATACAACTGTGG 15
RESULT 131
AAF48759
ID  AAF48759 standard; DNA; 15 BP.
XX
AC  AAF48759;
XX
XX
DT  30-MAR-2001 (first entry)
XX
DE  IGFBP3 oligonucleotide #2179.
XX
KW  Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW  cytostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
KW  skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW  IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW  growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW  keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW  hyperneovascular condition; hyperplasia; kidney disease;
KW  neovascular condition of the retina; ss.
XX
OS  Homo sapiens.
XX
XX  WO200078341-A1.
XX
PD  28-DEC-2000.
XX
XX  21-JUN-2000; 2000WO-AU000693.
XX
XX  21-JUN-1999; 99US-0140345P.
XX
PA  (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX  Wright CJ, Werther GA, Edmondson SR;
XX
XX  WPI; 2001-041421/05.
XX
XX  Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX  UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX  inhibits or reduces growth factor mediated cell proliferation and/or
XX  inflammation.
XX
PS  Example 7; Page 58; 201pp; English.
XX
XX  The present invention relates to a method for ameliorating the effects of
XX  skin disorders. The method comprises contacting the skin with an
XX  antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX  receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX  inhibiting or reducing growth factor mediated cell proliferation,
XX  inflammation and/or other disorders. The present sequence is an
XX  oligonucleotide which can be used to design the antisense
XX  oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX  F45161). The method is useful for ameliorating the effects of psoriasis,
XX  ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX  neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX  hyperneovascular condition such as a neovascular condition of the retina,
XX  brain or skin, growth factor-mediated malignancies, other sclerotic
XX  disease, kidney disease, hyperproliferation of the inside of blood
XX  vessels or any other hyperplasia
XX
SQ  Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
    Query Match      14.8%; Score 11.4; DB 1; Length 15;
    Best Local Similarity 92.3%; Pred. No. 1.1e+02;
    Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  19  GATACAACTGTGG 31
    |||||
Db  2  GATACAACTGTGG 14
    |||||

RESULT 132

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ADV37029
ID  ADV37029 standard; RNA; 15 BP.
XX
AC  ADV37029;
XX
DT  10-FEB-2005 (first entry)
XX
DE  Human anti-HER2 NCH ribozyme substrate sequence #908.
XX
XX  Enzymatic nucleic acid molecule; gene expression; down regulation;
XX  protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX  MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX  beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX  c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX  hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX  amberzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
XX  diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX  hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX  ss.
XX
OS  Homo sapiens.
XX
XX  WO200116312-A2.
XX
PD  08-MAR-2001.
XX
XX  30-AUG-2000; 2000WO-US023998.
XX
XX  31-AUG-1999; 99US-0151713P.
XX  27-SEP-1999; 99US-00406643.
XX  27-SEP-1999; 99US-0156236P.
XX  27-SEP-1999; 99US-0156467P.
XX  08-NOV-1999; 99US-00436430.
XX  06-DEC-1999; 99US-0169100P.
XX  29-DEC-1999; 99US-00474432.
XX  29-DEC-1999; 99US-0173612P.
XX  30-DEC-1999; 99US-00476387.
XX  04-FEB-2000; 2000US-00498824.
XX  20-MAR-2000; 2000US-00531025.
XX  14-APR-2000; 2000US-0197769P.
XX  23-MAY-2000; 2000US-00578223.
XX  09-AUG-2000; 2000US-00636385.
XX
PA  (RIBO-) RIBOZYME PHARM INC.
XX
XX  Mcswiggen J, Usman N, Blatt L, Reigelman L, Burgin A;
XX  Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX  Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX
XX  WPI; 2001-244406/25.
XX
XX  Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX  are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX  obesity and heart disease.
XX
PS  Example 7; Page 490; 717pp; English.
XX
XX  The present invention relates to the use of enzymatic nucleic acid
XX  molecules (e.g. ribozymes) to modulate gene expression. The invention of
XX  also methods for their use to down regulate or inhibit the expression of
XX  genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
XX  aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX  alpha (PKC alpha) beta-secretase (BACE), human epidermal growth factor
XX  receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX  presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX  nucleic acid molecules used to inhibit the expression of the said genes
XX  include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX  zinzyme, and/or DNazyme motifs. The methods of the invention are useful
XX  for treating cancer, in particular breast cancer, Alzheimer's disease,
XX  diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX  diseases, hepatitis B infections, and hepatitis and hepatocellular
XX  carcinoma. The enzymatic nucleic acid molecules can also be used as
XX  diagnostic tools to examine genetic drift and mutations within diseased

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CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a substrate/target sequence for an anti-HER2 NCH  
 CC ribozyme used in the examples of the present invention. Note: Some SEQ ID  
 CC Nos are repeated more than once in the specification, but these have  
 CC different sequences associated with them.

XX Sequence 15 BP; 3 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;

Best Local Similarity 69.2%; Pred. No. 1.1e+02;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 29 TGGAGTCTCTGGA 41

Db 1 UGGAGCCUCUGA 13

#### RESULT 133

AAL48040

ID AAL48040 standard; DNA; 15 BP.

XX AC

XX AC

XX 27-SEP-2002 (first entry)

XX Human CSF3 gene allele specific primer SEQ ID NO: 18.

XX Human; colony stimulating factor 3 (granulocyte); CSF3; SNP; isogene;  
 KW chromosome 17q11-12; single nucleotide polymorphism; immunostimulant;  
 KW neutropenia; promyelocytic leukaemia; haematological disorder;  
 KW gene therapy; PCR; primer; ss.

XX Homo sapiens.

XX WO200194364-A2.

XX 13-DEC-2001.

XX 11-JUN-2001; 2001WO-US018813.

XX 09-JUN-2000; 2000US-0210380P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Duda A, Kazemi A, Messer C, Sausker EA;

XX WPI; 2002-566435/60.

XX New variants of colony stimulating factor 3 (CSF3) isogenes, useful for  
 PT improving efficiency and reliability in the development of drugs for  
 PT treating diseases associated with CSF3 activity e.g. neutropenia.

XX Claim 17; Page 13; 68pp; English.

XX The present invention provides the protein, gene and cDNA sequences of  
 CC human colony stimulating factor 3 (granulocyte) CSF3. Also described are  
 CC single nucleotide polymorphisms (SNPs) identified within these sequences.  
 CC The sequences can be used in the treatment of neutropenia, promyelocytic  
 CC leukaemia and haematological disorders. The present sequence is an allele  
 CC specific primer used to isolate the coding sequences of the invention

XX Sequence 15 BP; 2 A; 1 C; 9 G; 2 T; 0 U; 1 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 AGACGGCTGGGAT 21

Db 1 AGAGGGCTGGGRT 15

#### RESULT 134

ABN80560/C

ID ABN80560 standard; DNA; 15 BP.

XX AC

XX AC

XX 19-JUL-2002 (first entry)

XX Human P450(cytochrome) oxidoreductase allele specific probe #26.

XX Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;  
 KW single nucleotide polymorphism; flavoprotein; enzyme; probe; ss.

XX Homo sapiens.

XX WO200226768-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-US030877.

XX 29-SEP-2000; 2000US-0236449P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Kazemi A, Kliem SE, Lanz EM, Messer C, Tanguay DA;

XX WPI; 2002-394236/42.

XX New genetic variants comprising haplotypes of the P450 (cytochrome)  
 PT oxidoreductase (POR) isogene, useful in improving the efficiency of drug  
 PT screening protocols for compounds targeting POR.

XX Claim 14; Page 14; 141pp; English.

XX The present invention provides the protein, gene and cDNA sequences of  
 CC human P450(cytochrome) oxidoreductase POR, and single nucleotide  
 CC polymorphisms (SNPs) identified therein. The sequences can be used to  
 CC haplotype the POR gene of an individual, and to establish whether POR is  
 CC a suitable target for drugs to treat cancer and disorders associated with  
 CC impaired protein synthesis in cells. The present sequence is an allele  
 CC specific probe for the coding sequences of the invention

XX Sequence 15 BP; 1 A; 6 C; 3 G; 4 T; 0 U; 1 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAAGCTGA 65

Db 15 AGCCAGCGGAGCTGA 1

#### RESULT 135

ADJ82348

ID ADJ82348 standard; DNA; 15 BP.

XX AC

XX AC

XX 06-MAY-2004 (first entry)

XX KLM5Y-encoding nucleotide #76.

XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;  
 KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;  
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;  
 KW myeloproliferative disease; blood vessel proliferative disease;  
 KW angiogenesis.

XX Synthetic.

XX WO2003045973-A2.

```

PD XX 05-JUN-2003.
PF XX 30-SEP-2002; 2002WO-US031165.
XX XX 28-NOV-2001; 2001US-0333476P.
PR XX (BECT ) BECTON DICKINSON & CO.
PA XX (HAAL/) HAALAND P D.
XX XX Dean C, Heidaran M, Spargo CA;
PI XX WPI; 2003-505179/47.
DR XX
XX XX New peptides having growth inhibitory action, useful for inhibiting tumor
PT or cancer cell proliferation, or for treating fibrotic disorders,
PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
PT disorders.
XX XX
PS Disclosure; SEQ ID NO 129; 48pp; English.
XX XX The invention relates to an isolated peptide or polypeptide (I) of no
CC more than about 50 amino acid residues which when contacted with cells in
CC which a platelet-derived growth factor receptor (PDGF-R) is activated in
CC an autocrine manner, inhibits the growth of these cells. The isolated
CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell
CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
CC muscle or bone cell. The peptides are also useful for treating fibrotic
CC disorders, myeloproliferative diseases, and blood vessel proliferative
CC (angiogenic) disorders. This sequence represents a possible nucleotide
CC encoding the P3 peptide.
XX XX
SQ Sequence 15 BP; 4 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 14.8%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCT 71
Db 1 AAGCTTATGTCCT 13
||||| |||||
RESULT 136
ADJ82364
ID ADJ82364 standard; DNA; 15 BP.
XX AC ADJ82364;
XX XX
DT 06-MAY-2004 (first entry)
XX DE KLMSY-encoding nucleotide #92.
XX XX
KW ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
KW myeloproliferative disease; blood vessel proliferative disease;
KW angiogenesis.
XX OS Synthetic.
XX XX
PN WO2003045973-A2.
XX XX
PD 05-JUN-2003.
XX XX
PF 30-SEP-2002; 2002WO-US031165.
XX XX 28-NOV-2001; 2001US-0333476P.
XX XX (BECT ) BECTON DICKINSON & CO.
XX XX (HAAL/) HAALAND P D.
XX XX Dean C, Heidaran M, Spargo CA;
XX XX WPI; 2003-505179/47.
XX XX
XX XX New peptides having growth inhibitory action, useful for inhibiting tumor
PT or cancer cell proliferation, or for treating fibrotic disorders,
PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
PT disorders.
XX XX
PS Disclosure; SEQ ID NO 129; 48pp; English.
XX XX The invention relates to an isolated peptide or polypeptide (I) of no
CC more than about 50 amino acid residues which when contacted with cells in
CC which a platelet-derived growth factor receptor (PDGF-R) is activated in
CC an autocrine manner, inhibits the growth of these cells. The isolated
CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell
CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
CC muscle or bone cell. The peptides are also useful for treating fibrotic
CC disorders, myeloproliferative diseases, and blood vessel proliferative
CC (angiogenic) disorders. This sequence represents a possible nucleotide
CC encoding the P3 peptide.
XX XX
SQ Sequence 15 BP; 4 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 14.8%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCT 71
Db 1 AAGCTTATGTCCT 13
||||| |||||
RESULT 137
ADJ82388
ID ADJ82388 standard; DNA; 15 BP.
XX AC ADJ82388;
XX XX
DT 06-MAY-2004 (first entry)
XX XX
DE KLMSY-encoding nucleotide #116.
XX XX
KW ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
KW myeloproliferative disease; blood vessel proliferative disease;
KW angiogenesis.
XX OS Synthetic.
XX XX
PN WO2003045973-A2.
XX XX
PD 05-JUN-2003.
XX XX
PF 30-SEP-2002; 2002WO-US031165.
XX XX 28-NOV-2001; 2001US-0333476P.
XX XX (BECT ) BECTON DICKINSON & CO.
XX XX (HAAL/) HAALAND P D.
XX XX Dean C, Heidaran M, Spargo CA;
XX XX WPI; 2003-505179/47.
XX XX

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XX New peptides having growth inhibitory action, useful for inhibiting tumor  
PT or cancer cell proliferation, or for treating fibrotic disorders,  
PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)  
PT disorders.

XX Disclosure; SEQ ID NO 169; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no  
CC more than about 50 amino acid residues which when contacted with cells in  
CC an autocrine manner, inhibits the growth of these cells. The isolated  
CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-  
CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-  
CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell  
CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,  
CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,  
CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,  
CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,  
CC muscle or bone cell. The peptides are also useful for treating fibrotic  
CC disorders, myeloproliferative diseases, and blood vessel proliferative  
CC (angiogenic) disorders. This sequence represents a possible nucleotide  
CC encoding the P3 peptide.

XX Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;  
Best Local Similarity 92.3%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AGCTGATGTCCT 71  
DB 1 AGCTGATGTCCT 13

RESULT 138  
ADJ82334  
ID ADJ82394 standard; DNA; 15 BP.  
XX AC ADJ82394;  
XX 06-MAY-2004 (first entry)  
XX KLMSY-encoding nucleotide #122.  
XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;  
XX carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;  
XX neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;  
XX myeloproliferative disease; blood vessel proliferative disease;  
XX angiogenesis.  
XX Synthetic.  
XX WO2003045973-A2.  
XX 05-JUN-2003.  
XX 30-SEP-2002; 2002WO-US031165.  
XX 28-NOV-2001; 2001US-0333476P.  
XX (BECT ) BECTON DICKINSON & CO.  
XX (HAAL/) HAALAND P D.  
XX Dean C, Heidaran M, Spargo CA;  
XX WPI; 2003-505179/47.  
XX New peptides having growth inhibitory action, useful for inhibiting tumor  
PT or cancer cell proliferation, or for treating fibrotic disorders,  
PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)  
PT disorders.

PS Disclosure; SEQ ID NO 175; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no  
CC more than about 50 amino acid residues which when contacted with cells in  
CC which a platelet-derived growth factor receptor (PDGF-R) is activated in  
CC an autocrine manner, inhibits the growth of these cells. The isolated  
CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-  
CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-  
CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell  
CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,  
CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,  
CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,  
CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,  
CC muscle or bone cell. The peptides are also useful for treating fibrotic  
CC disorders, myeloproliferative diseases, and blood vessel proliferative  
CC (angiogenic) disorders. This sequence represents a possible nucleotide  
CC encoding the P3 peptide.

XX Sequence 15 BP; 4 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;  
Best Local Similarity 92.3%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AGCTGATGTCCT 71  
DB 1 AGCTGATGTCCT 13

RESULT 139  
ADJ82380  
ID ADJ82380 standard; DNA; 15 BP.  
XX AC ADJ82380;  
XX 06-MAY-2004 (first entry)  
XX KLMSY-encoding nucleotide #108.  
XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;  
XX carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;  
XX neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;  
XX myeloproliferative disease; blood vessel proliferative disease;  
XX angiogenesis.  
XX Synthetic.  
XX WO2003045973-A2.  
XX 05-JUN-2003.  
XX 30-SEP-2002; 2002WO-US031165.  
XX 28-NOV-2001; 2001US-0333476P.  
XX (BECT ) BECTON DICKINSON & CO.  
XX (HAAL/) HAALAND P D.  
XX Dean C, Heidaran M, Spargo CA;  
XX WPI; 2003-505179/47.  
XX New peptides having growth inhibitory action, useful for inhibiting tumor  
PT or cancer cell proliferation, or for treating fibrotic disorders,  
PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)  
PT disorders.

XX Disclosure; SEQ ID NO 161; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no  
CC more than about 50 amino acid residues which when contacted with cells in  
CC which a platelet-derived growth factor receptor (PDGF-R) is activated in  
CC an autocrine manner, inhibits the growth of these cells. The isolated



CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys-Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.

XX  
SQ Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;  
Best Local Similarity 92.3%; Pred. NO. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCT 71  
|||||  
Db 1 AAGCTGATGTCCT 13

RESULT 140  
ADJ82332  
ID ADJ82332 standard; DNA; 15 BP.

XX AC ADJ82332;

XX DT 06-MAY-2004 (first entry)

XX DE KLMSY-encoding nucleotide #60.

XX SS; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; angiogenesis.

XX OS Synthetic.

XX PN WO2003045973-A2.

XX PD 05-JUN-2003.

XX PF 30-SEP-2002; 2002WO-US031165.

XX PR 28-NOV-2001; 2001US-0333476P.

XX PA (BECT ) BECTON DICKINSON & CO.  
(HAAL/) HAALAND P D.

XX PI Dean C, Heidaran M, Spargo CA;

XX WPI; 2003-505179/47.

XX New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.

XX PS Disclosure; SEQ ID NO 113; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGF-R) is activated in an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,

CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.

XX SQ Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 U; 0 Other;  
Query Match 14.8%; Score 11.4; DB 1; Length 15;  
Best Local Similarity 92.3%; Pred. NO. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCT 71  
|||||  
Db 1 AAGCTGATGTCCT 13

RESULT 141

ADJ82398

ID ADJ82398 standard; DNA; 15 BP.

XX AC ADJ82398;

XX DT 06-MAY-2004 (first entry)

XX DE KLMSY-encoding nucleotide #126.

XX SS; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; angiogenesis.

XX OS Synthetic.

XX PN WO2003045973-A2.

XX PD 05-JUN-2003.

XX PF 30-SEP-2002; 2002WO-US031165.

XX PR 28-NOV-2001; 2001US-0333476P.

XX PA (BECT ) BECTON DICKINSON & CO.  
(HAAL/) HAALAND P D.

XX PI Dean C, Heidaran M, Spargo CA;

XX WPI; 2003-505179/47.

XX New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.

XX PS Disclosure; SEQ ID NO 179; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGF-R) is activated in an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.

XX





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Db      15 GATACGCTCTNGAG 1
RESULT 144
ADE13694/c
ID      ADE13694 standard; DNA; 16 BP.
XX      AC      ADE13694;
XX      DT      29-JAN-2004 (first entry)
XX      DE      Oligonucleotide probe for diagnostic purposes seq id 26.
XX      KW      polymorphism detection; diagnostic;
XX      KW      single nucleotide polymorphism detection; SNP detection; array technology;
XX      KW      sequencing; hybridisation; ss; probe.
XX      OS      Synthetic.
XX      FH      Key      Location/Qualifiers
XX      modified_base 4
XX      FT      /*tag= a
XX      FT      /mod_base= OTHER
XX      FT      /note= "OTHER= Not described"
XX      modified_base 10
XX      FT      /*tag= b
XX      FT      /mod_base= OTHER
XX      FT      /note= "OTHER= Not described"
XX      US2003170711-A1.
XX      PD      11-SEP-2003.
XX      PP      25-FEB-2003; 2003US-00375504.
XX      PR      02-OCT-1997; 97US-0060673P.
XX      PR      18-AUG-1998; 98US-00136080.
XX      PR      18-JUL-2001; 2001US-0306229P.
XX      PR      08-MAY-2002; 2002US-00142729.
XX      PA      (BROW/) BROWN B D.
XX      PA      (RILE/) RILEY T A.
XX      PI      Brown BD, Riley TA;
XX      DR      WPI; 2003-830610/77.
XX      CC      New oligonucleotide for diagnostic purposes, e.g. detection of single
XX      CC      nucleotide polymorphisms, comprises universal and generic bases.
XX      PS      Disclosure; SEQ ID NO 26; 37pp; English.
XX      CC      The invention describes an oligonucleotide comprising 10-100 bases, in
XX      CC      which at least 2 bases are juxtaposed universal bases. Also disclosed is
XX      CC      a method for detecting a polymorphism in a genetic material comprising
XX      CC      contacting a DNA with the new oligonucleotide, and identifying whether
XX      CC      the oligonucleotide bound to the DNA. The novel oligonucleotide is used
XX      CC      for diagnostic purposes, e.g. detection of single nucleotide
XX      CC      polymorphisms (SNPs). It is also applicable in array technology,
XX      CC      sequencing, and hybridisation. The method increases the ability to
XX      CC      differentiate a single nucleotide polymorphism or a polymorphic site from
XX      CC      a normal site and allows the development of more efficient diagnostics
XX      CC      and therapeutics. This sequence represents an oligonucleotide of the
XX      CC      invention. Note: This sequence differs from the sequence given in the
XX      CC      examples of the invention.
XX      SQ      Sequence 16 BP; 3 A; 4 C; 3 G; 4 T; 0 U; 2 Other;
XX      Query Match      14.8%; Score 11.4; DB 1; Length 16;
XX      Best Local Similarity 80.0%; Pred. No. 1.1e+02;
XX      Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX      QY      19 GATACAACTCTGGAG 33

Db      15 GATACGCTCTNGAG 1
RESULT 145
ADM83304
ID      ADM83304 standard; DNA; 16 BP.
XX      AC      ADM83304;
XX      DT      03-JUN-2004 (first entry)
XX      DE      Probe 6 #2 used to identify mutations or polymorphisms.
XX      DE      Diagnosis; polymorphism detection; genetic disease; probe; ss.
XX      KW      Unidentified.
XX      OS      Key      Location/Qualifiers
XX      FH      misc_feature 4..5
XX      FT      /*tag= a
XX      FT      /note= "Linked via 3 numbers of 3-nitropyrrole group"
XX      misc_feature 12..13
XX      FT      /*tag= b
XX      FT      /note= "Linked via 2 numbers of 3-nitropyrrole group"
XX      US2003165888-A1.
XX      PD      04-SEP-2003.
XX      PP      08-MAY-2002; 2002US-00142729.
XX      PR      18-JUL-2001; 2001US-0306229P.
XX      PA      (BROW/) BROWN B D.
XX      PA      (RILE/) RILEY T A.
XX      PI      Brown BD, Riley TA;
XX      DR      WPI; 2003-787489/74.
XX      CC      New oligonucleotides useful as primers and probes for diagnosing
XX      CC      diseases, i.e. polymorphism in sample of genetic material, comprises
XX      CC      bases where some are juxtaposed universal bases.
XX      PS      Example 7; SEQ ID NO 35; 18pp; English.
XX      CC      The invention relates to novel oligonucleotide probes and primers
XX      CC      comprising universal and generic bases. The oligonucleotides of the
XX      CC      invention are useful as primers and probes for diagnosing diseases,
XX      CC      particularly in detecting polymorphism in a sample of genetic material
XX      CC      and for diagnosing a genetic disease in a patient. The present sequence is
XX      CC      a probe used to identify mutations or polymorphisms. This sequence is
XX      CC      used in the exemplification of the invention.
XX      SQ      Sequence 16 BP; 4 A; 4 C; 3 G; 5 T; 0 U; 0 Other;
XX      Query Match      14.8%; Score 11.4; DB 1; Length 16;
XX      Best Local Similarity 92.3%; Pred. No. 1.1e+02;
XX      Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX      QY      36 CTTCTGAGAGGTAA 48
XX      DB      1 CTTCTGAGAGGTAA 13

RESULT 146
ADM83291
ID      ADM83291 standard; DNA; 16 BP.
XX      AC      ADM83291;
XX      DT      03-JUN-2004 (first entry)

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XX DE Probe 6 #1 used to identify mutations or polymorphisms.
XX KW Diagnosis; polymorphism detection; genetic disease; probe; ss.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT misc_feature 4..5
XX FT /*tag= a
XX FT /note= "Linked via 3 numbers of 3-nitropyrrrole group"
XX FT 15..16
XX FT /*tag= b
XX FT /note= "Linked via 2 numbers of 3-nitropyrrrole group"
XX FN US2003165888-A1.
XX PD 04-SEP-2003.
XX PF 08-MAY-2002; 2002US-00142729.
XX PR 18-JUL-2001; 2001US-0306229P.
XX PR (BROW/) BROWN B D.
XX PA (RILEY/) RILEY T A.
XX PI Brown BD, Riley TA;
XX PX WPI; 2003-787489/74.
XX SQ Sequence 16 BP; 4 A; 4 C; 3 G; 5 T; 0 U; 0 Other;
XX Query Match 14.8%; Score 11.4; DB 1; Length 16;
XX Best Local Similarity 92.3%; Pred. No. 1.1e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 36 CTCTGAGAGGTAA 48
XX DB 1 CTCTGAGAGGTAA 13
XX RESULT 147
XX AAT18111
XX ID AAT18111 standard; DNA; 16 BP.
XX AC AAT18111;
XX XX
XX XX 30-AUG-1996 (first entry)
XX XX
XX XX M. kansasii species specific amplification primer. DI.
XX KW Species-specific amplification; M. kansasii; p6123; probe; pMK1-9;
XX KW strand displacement amplification; SDA; primers; Mycobacterium;
XX KW cross-react; Nocardia asteroides; Rhodococcus rhodochrous; ss.
XX XX
XX OS Synthetic.
XX XX
XX FN US5500341-A.
XX XX

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PD 19-MAR-1996.
XX 19-SEP-1994; 94US-00308892.
XX 19-SEP-1994; 94US-00308892.
XX (BECT ) BECTON DICKINSON CO.
XX PA Spears PA;
XX PI WPI; 1996-171042/17.
XX DR Primers for species-specific amplification of Mycobacterium kansasii -
XX PT detect double stranded target sequences with no cross-reactivity between
XX FT species.
XX PS Disclosure; Col 17; 15pp; English.
XX CC The sequences given in AAT18103-11 are primers which may be used in the
XX CC species-specific amplification of M. kansasii DNA. These primers bind to
XX CC a fragment, bases 51-220, of the clone p6123. p6123 is a cloned probe
XX CC which hybridises to all M. kansasii strains, including the subgroup which
XX CC is negative to binding with the probe pMK1-9 (M.Yang et al. 1993. J.
XX CC Clin. Microbid. 31, 2769-2772). These primers are pref. used in strand
XX CC displacement amplification (SDA). These primers showed a positive
XX CC reaction with 74 M. kansasii isolates tested, but did not cross react
XX CC with any other Mycobacterium species. In addition, these primers did not
XX CC cross-react with Nocardia asteroides or Rhodococcus rhodochrous. This
XX CC primer binds around bases 141-156 of the p6123 fragment
XX SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX Query Match 14.5%; Score 11.2; DB 1; Length 16;
XX Best Local Similarity 81.2%; Pred. No. 1.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 3 AACAGACGCGCTGGG 18
XX DB 1 AACTCGACGCGCTCGG 16
XX RESULT 148
XX ABS56009/c
XX ID ABS56009 standard; RNA; 16 BP.
XX AC ABS56009;
XX XX
XX DT 07-AUG-2003 (revised)
XX DT 07-JAN-2003 (first entry)
XX XX
XX DE West Nile virus genome, nucleotides 1-16.
XX XX Mutant replication-defective flavivirus; arthropod vector;
XX KW 3' stem-loop structure substitution; Dengue virus type 2; DEN2;
XX KW West Nile virus; WN; flavivirus-induced infection; dengue fever;
XX KW dengue haemorrhagic fever; dengue shock syndrome; virucide; ss.
XX OS West Nile virus.
XX XX
XX PN WO200274963-A1.
XX PD 26-SEP-2002.
XX PF 16-MAR-2001; 2001WO-US008686.
XX PR 16-MAR-2001; 2001WO-US008686.
XX XX (USSH ) US DEPT OF HEALTH.
XX PA Markoff L, Zeng L;
XX PI
XX XX WPI; 2002-750556/81.
XX XX

```

PT New mutant replicon-defective flavivirus having a genome with a 3' stem-  
 PT loop structure chimeric substitution useful as vaccine for treating  
 PT flavivirus-induced infection e.g. dengue fever, dengue hemorrhagic  
 PT fever/shock syndrome.

XX Example 3; Page 61; 67pp; English.

PS The present invention relates to a mutant replication-defective  
 XX flavivirus having a genome with a 3' stem-loop structure substitution,  
 CC and being defective for replication in an arthropod vector that transmits  
 CC flavivirus to humans. The genome is selected from a first flavivirus and  
 CC the 3' stem-loop structure from a second flavivirus, where the first  
 CC flavivirus is different from the second. For example the first flavivirus  
 CC may be Dengue virus type 2 (DENV2) and the second flavivirus may be West  
 CC Nile virus (WNV). The mutant replicon-defective flavivirus is useful as a  
 CC vaccine for treating flavivirus-induced infections, particularly dengue  
 CC fever or dengue hemorrhagic fever/shock syndrome. The present sequence  
 CC represents a part of the WNV genome used to construct a mutant replication  
 CC -defective flavivirus in the examples of the present invention. (Updated  
 CC on 07-AUG-2003 to correct OS field.)

XX Sequence 16 BP; 7 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 14.5%; Score 11.2; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 1.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 26 CTCTGGAGTCTCTGA 41

Db 16 CTCTGTGTCTCTATGA 1

#### RESULT 149

ABK29916/c

ID ABK29916 standard; DNA; 16 BP.

XX ABK29916;

XX 23-APR-2002 (first entry)

XX Androgen receptor wild type HLH-3 sequence.

XX Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;  
 KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;  
 KW vanH promoter; androgen receptor promoter; AR promoter;  
 KW human epidermal growth factor receptor 2 promoter; her2 promoter;  
 KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;  
 KW colon cancer; immunological disorder; prostate cancer; cytostatic;  
 KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;  
 KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;  
 KW gene expression modulator; multiple sclerosis; MS;  
 KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;  
 KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;  
 KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;  
 KW transgenic; ss.

XX Homo sapiens.

XX WO200194600-A2.

XX 13-DEC-2001.

XX 06-JUN-2001; 2001WO-US018343.

XX 06-JUN-2000; 2000US-0209549P.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EP;

PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;

PI Lim MY, Bruce TW;

XX WPI; 2002-130595/17.

XX New nucleic acid regulatory sequences, which are able to regulate  
 PT expression of a gene operably linked to a promoter, useful for regulating  
 PT the expression of transgenes and for treating e.g., cancer and  
 PT immunological diseases.

XX Claim 13; Page 60; 95pp; English.

PS The invention describes an isolated nucleic acid regulatory sequence for  
 XX a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci  
 CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human  
 CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase  
 CC (Bla) promoter. Transcription regulatory sequences may be used to  
 CC regulate expression of the endogenous, autologous or heterologous genes  
 CC operably linked to the promoter, and may be incorporated into  
 CC heterologous nucleic acid constructs for use in regulated expression of  
 CC transgenes. Regulated expression of cyclin D1 can be used in cancer  
 CC therapies, such as breast, colon or pancreatic cancers and familial  
 CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter  
 CC may be used in the treatment of immunological disorders, such as  
 CC autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus  
 CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid  
 CC arthritis. Regulated expression of genes under the control of the HBV  
 CC (hepatitis B)-specific core, pre-S and X promoters can be used in the  
 CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,  
 CC hepatocellular carcinoma, and in the regulated expression of liver cell-  
 CC specific genes. Regulated expression of the vanH gene promoter can be  
 CC used in treatment of Enterococcus infection, while regulated expression  
 CC of the androgen receptor gene can be used in the treatment of prostate  
 CC cancer. This sequence represents a primer used in the invention to  
 CC determine the functions of regions within the selected promoters,  
 CC described in the method of the invention

XX Sequence 16 BP; 2 A; 9 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 14.5%; Score 11.2; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 1.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 38 CTGAGAGGTAAAGAGC 53

Db 16 CTGGAGGTGGAGAGC 1

#### RESULT 150

AAU56970/c

ID AAL56970 standard; DNA; 16 BP.

XX AAL56970;

XX 11-MAR-2004 (first entry)

XX Human hypoxia-inducible factor-1 alpha antisense oligo #66.

XX HTF-1alpha; hypoxia-inducible factor-1 alpha; human; antisense; cancer;  
 KW pre-eclampsia; cytostatic; gynaecological; antiinflammatory; neutropic;  
 KW neuroprotective; ss.

XX Homo sapiens.

XX WO2003085110-A2.

XX 16-OCT-2003.

XX 04-APR-2003; 2003WO-IB001758.

XX 05-APR-2002; 2002US-0370126P.

XX (CURE-) CUREON AS.

XX Thru CA, Hog AM, Kristjansen PEG;

XX WPI; 2003-812728/76.

XX PT New oligonucleotide that modulates hypoxia-inducible factor-1alpha,  
 PT useful for treating e.g. cancer or Alzheimer's disease.

XX PS Claim 1; Page 42; Opp; English.

XX CC The present invention relates to compounds capable of modulating hypoxia-  
 CC inducible factor-1alpha (HIF1a). The compounds are used to treat patients  
 CC with, or at risk of developing, cancer (e.g. of breast, prostate,  
 CC pancreas, lung), pre-eclampsia, inflammatory bowel disease or Alzheimer's  
 CC disease, for modulating angiogenesis, proliferation of erythrocytes and  
 CC other cells, iron, glucose and energy metabolism, pH regulation, tissue  
 CC invasion, apoptosis, multiple drug resistance, cellular stress responses,  
 CC and matrix metabolism, especially apoptosis where modulation is  
 CC sensitivity to an apoptotic stimulus, particularly a chemotherapeutic  
 CC agent and for inhibiting proliferation of cells (especially cancer cells)  
 CC in vitro. The present sequence is an antisense oligonucleotide against  
 CC HIF1alpha identified in the exemplification of the invention

XX SQ Sequence 16 BP; 0 A; 3 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 14.5%; Score 11.2; DB 1; Length 16;  
 Best Local Similarity 81.2%; Pred. No. 1.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 47 AAGAGCCAGCGAGC 62  
 ||| |||||  
 Db 16 AAGACACAGCGAGC 1

RESULT 151  
 ABQ86793/C  
 ID ABQ86793 standard; cDNA; 11 BP.

XX AC ABQ86793;

XX DT 10-SEP-2002 (first entry)

XX DE Human skin stress/ageing related EST SEQ ID NO 548.

XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO200253773-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015178.

XX PR 03-JAN-2001; 2001DE-01000121.

XX PA (HENKEL ) HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-528865/56.

XX PT Identifying genes involved in skin stress and aging, useful e.g. in  
 PT screening for cosmetic or therapeutic agents, based on differential gene  
 PT expression.

XX PS Claim 8; Page 59; 325pp; German.

XX CC The invention relates to identifying (M1) genes in vitro that, in humans  
 CC or animals, are important for skin ageing and/or skin stress by serial  
 CC analysis of gene expression between mixtures of transcribed and  
 CC optionally translated, genetically encoded factors (A) obtained from  
 CC young and aged skin, to identify that genes that show strong differential  
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
 CC useful for: identifying markers of skin ageing and/or stress; determining  
 CC skin ageing and/or stress; and identifying or determining the effects of  
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present

CC sequence is one of a group of human skin ageing/stress related expressed  
 CC sequence tags (ABQ86246-ABQ87680) of the invention

XX SQ Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 14.3%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 86;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATACAACTCTG 30  
 |||||  
 Db 11 ATACAACTCTG 1

RESULT 152  
 ABV71507/C  
 ID ABV71507 standard; cDNA; 11 BP.

XX AC ABV71507;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 9293.

XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENKEL ) HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX PT In vitro identification of skin-expressed genes, useful for determining  
 PT homeostasis and identifying cosmetic or pharmaceutical agents against  
 PT e.g. skin cancer.

XX PS Claim 24; Page 299; 1345pp; German.

XX CC The invention relates to in vitro identification (M1) of genes expressed  
 CC in the skin of humans or animals by subjecting a mixture of genetically  
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
 CC so as to identify skin-expressed genes and quantify their expression.  
 CC (M1) is useful for identifying genes involved in skin homeostasis; to  
 CC determine skin homeostasis and to test agent (A) that maintains or  
 CC promotes skin homeostasis or that can be used for treating skin  
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
 CC skin. The present sequence is that of a human expressed sequence tag  
 CC (EST) of the invention

XX SQ Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 14.3%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 86;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATACAACTCTG 30  
 |||||  
 Db 11 ATACAACTCTG 1

```

RESULT 153
ABV64086/c
ID ABV64086 standard; cDNA; 11 BP.
XX
AC ABV64086;
XX
DT 21-OCT-2002 (first entry)
XX
XX Human skin EST 1872.
XX
XX Human; skin; dermatological; vulnery; antipeoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX
XX Disclosure; Page 76; 1345pp; German.
XX
XX The invention relates to in vitro identification (MI) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (MI) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
XX Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 ATACAACTCTG 30
DB 11 ATACAACTCTG 1
|||||
RESULTS 154
ACCS8751
ID ACC58751 standard; DNA; 11 BP.
XX
AC ACC58751;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-restenosis phosphorothioate oligonucleotide hairpin loop region.
XX
KW Anti-restenosis; vasotropic; phosphorothioate; ss.
XX

```

```

OS Synthetic.
XX
XX Key Location/Qualifiers
FH stem_loop 1..11
FT /*tag= a
FT modified_base 1..11
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate nucleotides"
XX
XX WO2003035666-A2.
XX
XX 01-MAY-2003.
XX
XX 25-OCT-2002; 2002WO-EP011964.
XX
XX 26-OCT-2001; 2001GB-00025746.
XX
XX (CATH-) CATHNET-SCI HOLDING AS.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Andersen E, Le Doan T, Lamidey L;
XX
XX WPI; 2003-504990/47.
XX
XX Anti-restenosis agent for treating restenosis e.g. in smooth muscle
XX tissue, comprises a phosphorothioate-modified oligonucleotide comprising
XX one hairpin loop and a dt or dg releasing group.
XX
XX Claim 5; Page 32; 39pp; English.
XX
XX The present sequence comprises the 5' or (preferably) 3' terminal hairpin
XX loop region of anti-restenosis phosphorothioate oligonucleotides of the
XX invention (see also ACC58756-57). A claimed oligonucleotide for treating
XX restenosis, e.g. in smooth muscle tissue, comprises a phosphorothioate
XX modified oligonucleotide that includes at least one hairpin loop, a dt or
XX dg releasing group and at least one multi-guanosine sequence. The
XX oligonucleotide has a long active life in vivo due to the presence of the
XX hairpin loop. It may be used as, or in, a coating on a device for
XX implantation into the body, e.g. a stent for use in percutaneous
XX transluminal coronary angioplasty (PTCA)
XX
XX Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
XX
Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 CAGCGAAGCTG 64
DB 1 CAGCGAAGCTG 11
|||||
RESULTS 155
AAQ24027/c
ID AAQ24027 standard; DNA; 12 BP.
XX
XX AAQ24027;
XX
XX 25-MAR-2003 (revised)
DT 21-SEP-1992 (first entry)
XX
XX Herpesvirus inhibiting antisense oligonucleotide.
XX
XX HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster;
KW Epstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.
XX
XX Synthetic.
XX
XX WO9205284-A.
XX
XX 02-APR-1992.
XX

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PF 18-SEP-1991; 91WO-US006646.
XX
PR 21-SEP-1990; 90US-00586185.
XX
PA (UYMA-) UNIV MARYLAND BALTIMORE.
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Aurelian L, Tso P;
XX
DR WPI; 1992-132145/16.
XX
PT New anti-sense oligo:nucleotide(s) for inhibiting HSV - also used for
PT diagnosis and for inhibiting HIV activation by herpes virus.
PS Claim 1; Page 38; 77pp; English.
XX
XX The sequence is that of an antisense oligonucleotide which can be used
CC for inhibiting growth or replication of herpesviruses. It corresponds to
CC an antisense sequence of a herpesvirus site, pref. in a gene that is
CC essential for synthesising nucleic acids e.g. the immediate early genes
CC or Vmw65. It can be prepd. by solid phase triester or phosphor- amidite
CC chemistry or by recombinant DNA techniques. It can be used for treating
CC infection by herpesviruses, e.g. herpes simplex type 1 (HSV-1) and type 2
CC (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cytomegalovirus
CC (CMV), human herpesvirus 6 (HHV-6) and 7 (HHV-7). In addition, the
CC inhibition of herpesvirus growth or replication may indirectly forestall
CC the progression of events from HIV exposure to the clinical manifestation
CC of AIDS. It may also be useful in the detection, diagnosis and
CC manipulation of herpes virus. See also AAQ23764-Q23788 and AAQ24014-
CC Q24044. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 12 BP; 4 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 14.3%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 TGGAGTCCTCT 39
Db 11 TGGAGTCCTCT 1

RESULT 156
ABI20955/c
ID ABI20955 standard; DNA; 12 BP.
XX
AC ABI20955;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 320928 for detecting SNP TSC0029975.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DB-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 14594; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

Query Match 14.3%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GAGAGGTAAG 50
Db 12 GAGAGGTAAG 2

RESULT 157
ABC14587/c
ID ABC14587 standard; DNA; 13 BP.
XX
AC ABC14587;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 14594 for detecting SNP TSC0003290.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DB-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 14594; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

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CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 1 Other;  
 Query Match 14.3%; Score 11; DB 1; Length 13;  
 Best Local Similarity 84.6%; Pred. No. 1e+02;  
 Matches 11; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 41 AGAGGTTAAAGC 53  
 DB 13 AGAAGTAAGAGY 1  
 ||| |||||

RESULT 158  
 ABF82001/c  
 ID ABF82001 standard; DNA; 13 BP.

XX AC ABF82001;

XX DT 22-FEB-2002 (first entry)

DE DE Oligonucleotide SEQ ID NO 181998 for detecting SNP TSC0044987.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX PS Claim 1; SEQ ID NO 181998; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 14.3%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAA 49  
 |||||

Db 12 TGAGAGGTAAA 2

RESULT 159

ABF82000  
 ID ABF82000 standard; DNA; 13 BP.

XX AC ABF82000;

XX DT 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 181997 for detecting SNP TSC0044987.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX PS Claim 1; SEQ ID NO 181997; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 6 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 14.3%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAA 49  
 |||||

Db 2 TGAGAGGTAAA 12

RESULT 160

ABH24941/c  
 ID ABH24941 standard; DNA; 13 BP.

XX AC ABH24941;

XX DT 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 224918 for detecting SNP TSC0054826.



KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 224918; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 1 A; 4 C; 0 G; 8 T; 0 U; 0 Other;  
 Query Match 14.3%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 41 AGAGGTAAGA 51  
 DB 12 AGAGGTAAGA 2  
 RESULT 161  
 ABC14586  
 ID ABC14586 standard; DNA; 13 BP.  
 XX ABC14586;  
 XX 20-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 14593 for detecting SNP TSC0003290.  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 14593; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 1 Other;  
 Query Match 14.3%; Score 11; DB 1; Length 13;  
 Best Local Similarity 84.6%; Pred. No. 1e+02;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 41 AGAGGTAAGAGC 53  
 DB 1 AGAGGTAAGAGY 13  
 RESULT 162  
 ABH24940  
 ID ABH24940 standard; DNA; 13 BP.  
 XX ABH24940;  
 XX 22-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 224917 for detecting SNP TSC0054826.  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 224917; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
 SQ Sequence 13 BP; 8 A; 0 C; 4 G; 1 T; 0 U; 0 Other;  
 Query Match 14.3%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGAGGTAAGA 51  
 Db 2 AGAGGTAAGA 12  
 |||||

RESULT 163  
 AAA26129  
 ID AAA26129 standard; DNA; 14 BP.

XX  
 AC AAA26129;

XX  
 DT 19-JUL-2000 (first entry)

XX  
 DE Oestrogen receptor hairpin ribozyme target sequence SEQ ID NO:2627.

XX  
 KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.

XX  
 OS Homo sapiens.

XX  
 PN WO9954459-A2.

XX  
 PD 28-OCT-1999.

XX  
 PF 19-APR-1999; 99WO-US008547.

XX  
 PR 20-APR-1998; 98US-0082404P.

XX  
 PR 23-JUN-1998; 98US-00103636.

XX  
 PA (RIBO-) RIBOZYME PHARM INC.

XX  
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;

XX  
 DR WPI; 2000-013248/01.

XX  
 PT New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.

XX  
 PS Claim 79; Page 99; 148pp; English.

XX  
 CC The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphorodi(thio)ate  
 CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research

CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention

XX  
 SQ Sequence 14 BP; 2 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 14.3%; Score 11; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACGGCTCTGGG 19

Db 3 ACGGCTCTGGG 13

RESULT 164

ABT13117

ID ABT13117 standard; DNA; 14 BP.

XX  
 AC ABT13117;

XX  
 DT 30-JAN-2003 (first entry)

XX  
 DE Fanconi anaemia FANCD intron/exon junction oligo SEQ ID NO 20.

XX  
 KW Cytostatic; dermatological; vasotropic; anti-anaemic; FA pathway defect;  
 KW Fanconi anaemia protein complex; FANCD; DNA repair; Cockayne's syndrome;  
 KW cell cycle abnormality; Fanconi anaemia; ataxia telangiectasia; cancer;  
 KW Bloom's syndrome; Hereditary non-polyposis colon cancer; gene therapy;  
 KW Xeroderma pigmentosum; ds.

XX  
 OS Unidentified.

XX  
 PN WO200236761-A2.

XX  
 PD 10-MAY-2002.

XX  
 PF 02-NOV-2001; 2001WO-US045561.

XX  
 PR 03-NOV-2000; 2000US-0245756P.

XX  
 PA (DAND ) DANA FARBER CANCER INST INC.

XX  
 PI D'andrea AD, Taniguchi T, Timmers C, Grompe M;

XX  
 DR WPI; 2002-519251/55.

XX  
 PT Novel isolated Fanconi anemia protein complex polypeptide, termed FANCD2,  
 PT useful for treating Fanconi anemia pathway defect in cell target or for  
 PT treating patient with defective FANCD2 gene.

XX  
 PS Claim 7; Page 54; 103pp; English.

XX  
 CC The invention relates to an isolated Fanconi anaemia protein complex  
 CC (FANCD2) polypeptide. The FANCD2 protein comprises a sequence of 1472  
 CC amino acids fully defined in the specification, its 90% identical  
 CC sequence, a sequence encoded by a polynucleotide that is at least 90%  
 CC identical to sequences given in specification such as a 5127 base pair  
 CC sequence, or a fragment which is at least 50 amino acids in length. The  
 CC FANCD2 protein is useful for treating a FA pathway defect in a cell  
 CC target or for treating a patient with a defective FANCD2 gene. The FANCD2  
 CC gene is useful for making a recombinant expression vector. The FANCD2  
 CC protein and its gene are useful as a novel target for therapeutic  
 CC development, and in diagnostic test and screening assays for diseases  
 CC associated with DNA repair and cell cycle abnormalities such as Fanconi  
 CC anaemia, Bloom's syndrome, Cockayne's syndrome, Hereditary non-polyposis

CC angioplatic restenosis. By inhibiting CETP, the levels of HDL and low  
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered  
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).  
 CC The HH ribozymes can also be used diagnostically to study genetic drift  
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH  
 CC ribozymes target specific regions of the CETP gene, they have low non-  
 CC specific activity  
 XX  
 SQ Sequence 15 BP; 5 A; 3 C; 4 G; 0 T; 3 U; 0 Other;  
 Query Match 14.3%; Score 11; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 33 GTCCTCTGAGA 43  
 Db 15 GTCCTCTGAGA 5  
 |||||  
 RESULT 167  
 AAZ64343/c  
 ID AAZ64343 standard; RNA; 15 BP.  
 XX  
 AC AAZ64343;  
 XX  
 DT 28-MAR-2000 (first entry)  
 XX  
 DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 8121.  
 XX  
 KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;  
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;  
 KW autoimmune disease; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO9955847-A2.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 26-APR-1999; 99WO-US009027.  
 XX  
 PR 27-APR-1998; 98US-0083217P.  
 XX  
 PR 18-SEP-1998; 98US-0100842P.  
 PR 25-FEB-1999; 99US-00257608.  
 PR 23-MAR-1999; 99US-00274553.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;  
 XX  
 DR WPI; 2000-062023/05.  
 XX  
 PT Novel ribozymes for the treatment of diseases and conditions related to  
 PT hepatitis C infection.  
 XX  
 PS Claim 1; Page 89; 123pp; English.  
 XX  
 CC The present sequence represents the preferred target sequence of an  
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in  
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme  
 CC target sites using a computer folding algorithm and regions of the mRNA  
 CC which did not form secondary folding structures and contained potential  
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to  
 CC target these sites and their activities optimised by either varying the  
 CC length of the binding arms or by modification to prevent degradation by  
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or  
 CC viral replication, and are used to treat diseases associated with  
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and  
 CC hepatocellular carcinoma. The ribozymes may be used in combination with  
 CC interferon to treat HCV infection, other infectious diseases, autoimmune  
 CC diseases, and cancer  
 XX

SQ Sequence 15 BP; 4 A; 3 C; 3 G; 0 T; 5 U; 0 Other;  
 Query Match 14.3%; Score 11; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 45 GTAAAGAGCCA 55  
 Db 13 GTAAAGAGCCA 3  
 |||||  
 RESULT 168  
 AAZ64344/c  
 ID AAZ64344 standard; RNA; 15 BP.  
 XX  
 AC AAZ64344;  
 XX  
 DT 28-MAR-2000 (first entry)  
 XX  
 DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 8123.  
 XX  
 KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;  
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;  
 KW autoimmune disease; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO9955847-A2.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 26-APR-1999; 99WO-US009027.  
 XX  
 PR 27-APR-1998; 98US-0083217P.  
 PR 18-SEP-1998; 98US-0100842P.  
 PR 25-FEB-1999; 99US-00257608.  
 PR 23-MAR-1999; 99US-00274553.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;  
 XX  
 DR WPI; 2000-062023/05.  
 XX  
 PT Novel ribozymes for the treatment of diseases and conditions related to  
 PT hepatitis C infection.  
 XX  
 PS Claim 1; Page 89; 123pp; English.  
 XX  
 CC The present sequence represents the preferred target sequence of an  
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in  
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme  
 CC target sites using a computer folding algorithm and regions of the mRNA  
 CC which did not form secondary folding structures and contained potential  
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to  
 CC target these sites and their activities optimised by either varying the  
 CC length of the binding arms or by modification to prevent degradation by  
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or  
 CC viral replication, and are used to treat diseases associated with  
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and  
 CC hepatocellular carcinoma. The ribozymes may be used in combination with  
 CC interferon to treat HCV infection, other infectious diseases, autoimmune  
 CC diseases, and cancer  
 XX  
 SQ Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;  
 Query Match 14.3%; Score 11; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 45 GTAAAGAGCCA 55  
 |||||

CC colon cancer, ataxia telangiectasia and Xeroderma pigmentosum. The FANCD2  
 CC gene is useful in producing probes and primers for screening patients in  
 CC genetic based test, for diagnosing Fanconi anaemia and cancer, for  
 CC preparing an experimental mouse model for use in screening new  
 CC therapeutics for treating conditions involving defective DNA repair, and  
 CC in gene therapy methods. A recombinant vector containing the FANCD2 gene  
 CC of the invention is useful in gene therapy. This polynucleotide sequence  
 CC represents a FANCD intron/exon junction oligonucleotide relating to the  
 CC invention

XX Sequence 14 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
 SQ

Query Match 14.3%; Score 11; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 AGGTAAAGAGC 53  
 Db 2 AGGTAAAGAGC 12  
 |||||

RESULT 165  
 ADC42354  
 ID ADC42354 standard; DNA; 14 BP.  
 XX AC ADC42354;  
 AC  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human FANCD exon 12 5'-donor site SEQ ID NO:19.  
 XX  
 KW human; cancer; Fanconi Anaemia; FA; BRCA; cytostatic; microarray;  
 KW chemosensitising; ds.  
 KW  
 OS Homo sapiens.  
 XX  
 XX WO2003039327-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 06-JUN-2002; 2002WO-US018153.  
 XX  
 PR 02-NOV-2001; 2001US-00998027.  
 PR  
 PR 02-NOV-2001; 2001WO-US045561.  
 XX  
 XX (DAND ) DANA FARBER CANCER INST.  
 PA (UFOR-) UNIV OREGON HEALTH SCI.  
 XX  
 XX D'andrea AD, Taniguchi T, Timmers C, Grompe M, Fox EA;  
 PI  
 XX WPI; 2003-441436/41.  
 DR  
 XX  
 PT Diagnosing or determining cancer or increased risk of cancer in a  
 PT patient, by testing Fanconi Anemia/BRCA pathway gene or protein for a  
 PT cancer-associated defect, that indicates cancer or increased risk of  
 PT cancer.

XX  
 XX Example 4; SEQ ID NO 20; 160pp; English.  
 PS  
 XX The invention relates to a novel method of diagnosing or determining if a  
 CC patient has cancer or is at increased risk of cancer, involving testing a  
 CC Fanconi Anaemia (FA)/BRCA pathway gene or protein for the presence of a  
 CC cancer-associated defect, where the presence of one or more cancer-  
 CC associated defects is indicative of cancer or an increased risk of cancer  
 CC in the patient. The method of the invention has cytostatic activity. The  
 CC method is useful for determining if a patient has cancer, or is at  
 CC increased risk of developing cancer, e.g. breast, ovarian or prostate  
 CC cancer. A microarray of the invention is useful for determining if a  
 CC patient has cancer, or is at increased risk of developing cancer, by  
 CC hybridising a nucleic acid sample to the nucleic acid sequences from the  
 CC array, and detecting the presence of mutations in FA/BRCA pathway genes  
 CC in the nucleic acid sample from the patient, where detecting the presence  
 CC of mutations is indicative of a patient who has cancer, or is at

CC increased risk of developing cancer. A method of the invention is useful  
 CC for screening a chemosensitising agent, and the agent obtained is used in  
 CC the exemplification of the invention.

XX Sequence 14 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
 SQ

Query Match 14.3%; Score 11; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 AGGTAAAGAGC 53  
 Db 2 AGGTAAAGAGC 12  
 |||||

RESULT 166  
 AAT49756/C  
 ID AAT49756 standard; RNA; 15 BP.  
 XX AC AAT49756;  
 AC  
 DT 02-MAR-1997 (first entry)  
 XX  
 DE Human CERP HH ribozyme target sequence #906.  
 XX  
 KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;  
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;  
 KW reverse cholesterol transport; high density lipoprotein; therapy; CERP;  
 KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;  
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;  
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;  
 KW LDL; ss.  
 KW  
 OS Homo sapiens.  
 XX  
 XX WO9620279-A1.  
 XX  
 PD 04-JUL-1996.  
 XX  
 PF 11-DEC-1995; 95WO-US016000.  
 XX  
 PR 23-DEC-1994; 94US-00363240.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;  
 XX WPI; 1996-321852/32.  
 XX  
 PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -  
 PT useful for preventing or treating initial development, progression or  
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.  
 XX  
 PS Claim 4; Page 31; 72pp; English.  
 XX  
 CC AAT49608-T49863 represent target sequences for the human cholesterol  
 CC ester transfer protein (CERP) hammerhead (HH) ribozymes (see AAT49881-  
 CC T50137). CERP is a 74 kD glycoprotein that facilitates neutral lipid  
 CC transfer between plasma lipoproteins. The numbering of the targets refers  
 CC to the position of the cleavage site in full length CERP. The ribozyme  
 CC binds to 5 nucleotides either side of this site, provided the sequence  
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the  
 CC gene encoding CERP, thereby blocking synthesis and/or expression of the  
 CC mRNA. By inhibiting CERP, the reverse cholesterol transport (RCT) pathway  
 CC can be inhibited (or eliminated) thereby preventing the reduction in size  
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,  
 CC and therefore increasing HDL levels. The ribozymes can be used to treat  
 CC conditions associated with abnormal levels of CERP, specifically familial  
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,  
 CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,  
 CC vascular complications of diabetes, transplant, atherectomy and

```

Db          11  GTRAGGCCA 1
RESULT 169
AAD25954
ID  AAD25954 standard; DNA; 15 BP.
XX
XX  AAD25954;
AC  AAD25954;
XX
XX  26-MAR-2002 (first entry)
DT
XX
XX  ASO probe #7 to detect human P14 gene polymorphisms.
DE
XX
XX  Human; protease inhibitor; P14; kallistatin; therapy; polymorphic site;
KW  PS; haplotyping; genotyping; acute pancreatitis; drug screening;
KW  antiinflammatory; chromosome 14q31-q32.1; probe; ss.
XX
XX  Homo sapiens.
OS
XX  WO200179227-A2.
FN
XX  25-OCT-2001.
PD
XX  13-APR-2001; 2001WO-US012255.
XX
XX  13-APR-2000; 2000US-0196990P.
XX
XX  (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX  Choi JY, Koshiy B, Sanchis A;
PI
XX  WPI; 2002-075060/10.
DR
XX
XX  Genotyping protease inhibitor 4 gene of individual for determining
PT  haplotype of individual, involves determining identity of nucleotide pair
PT  at specific polymorphic sites for two copies of gene.
XX
XX  Claim 16; Page 13; 79pp; English.
XX
XX  The present invention relates to genotyping protease inhibitor (PI) 4
CC  (kallistatin) gene of an individual, involves determining for the two
CC  copies of the P14 gene present in the individual, the identity of the
CC  nucleotide pair at one or more polymorphic sites. P14 gene is located on
CC  chromosome 14q31-q32.1. Genotyping is useful for determining if an
CC  individual has a haplotype or haplotype pairs defined in the
CC  specification. Haplotyping is useful for improving the efficacy and
CC  reliability of several steps in the discovery and development of drugs
CC  for treating diseases associated with P14 activity, e.g. acute
CC  pancreatitis, to validate P14 as a candidate agent for treating a
CC  specific condition or disease predicted to be associated with P14
CC  activity, and in the design of clinical trials of candidate drugs for
CC  treating a specific condition or disease predicted to be associated with
CC  P14 activity. The P14 gene is useful in studying the expression and
CC  function of P14, and in expressing P14 protein for use in screening for
CC  candidate drugs to treat diseases related to P14 activity. The present
CC  sequence is a ASO (allele-specific oligonucleotide) probe to detect human
CC  P14 gene polymorphisms
XX
XX  Sequence 15 BP; 2 A; 4 C; 4 G; 4 T; 0 U; 1 Other;
SQ
Query Match      14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      61  GCTGATGCTCTGT 73
      |||:|||||
      3  GCAGAGTCTCTGT 15

RESULT 170
ABL88306/C
ID  ABL88306 standard; DNA; 15 BP.
XX
XX
AC  ABL88306;
XX
XX  20-MAY-2002 (first entry)
DT
XX
XX  Human CHRNA allele-specific oligonucleotide (ASO) primer, SEQ ID NO:40.
DE
XX
XX  Human; cholinergic receptor nicotinic epsilon polypeptide; CHRNA;
KW  chromosome 17p13-12; acetylcholine receptor; AChR;
KW  neuromuscular junction; skeletal muscle; postnatal development;
KW  congenital myasthenic syndrome; CMS; haplotyping; genotyping; haplotype;
KW  genetic variant; single nucleotide polymorphism; SNP; gene therapy;
KW  drug screening; allele-specific oligonucleotide; ASO; primer; ss.
XX
XX  Homo sapiens.
OS
XX  WO200198316-A2.
FN
XX  27-DEC-2001.
PD
XX  20-JUN-2001; 2001WO-US019835.
XX
XX  20-JUN-2000; 2000US-0212870P.
XX
XX  (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX  Amaro E, Bieganski KM, Klien SE, Koshiy B, Tanguay DA;
PI
XX  WPI; 2002-130787/17.
DR
XX
XX  Novel genetic variants of cholinergic receptor, nicotinic, epsilon
PT  polypeptide gene useful in studying expression and function of the
PT  protein, and for screening drugs to treat diseases e.g. congenital
PT  myasthenic syndrome.
XX
XX  Claim 17; Page 14; 104pp; English.
XX
XX  The invention relates to a method for haplotyping the cholinergic
CC  receptor, nicotinic, epsilon polypeptide (CHRNA) gene (ABL88268) of an
CC  individual, and also describes 17 novel polymorphic sites within the
CC  human CHRNA gene. The CHRNA gene is located on chromosome 17p13-12 and
CC  contains 12 exons which encode a 493 amino acid protein (AB49112). The
CC  CHRNA protein is one of the 5 subunits of mammalian acetylcholine
CC  receptors (AChRs) found at neuromuscular junctions in juveniles and
CC  adults, and is essential for the normal postnatal development of skeletal
CC  muscle. Mutations in the CHRNA gene are associated with congenital
CC  myasthenic syndrome (CMS). CHRNA gene sequences can therefore be used in
CC  gene therapy. The CHRNA gene is also useful for studying the expression
CC  and function of CHRNA, and in expressing CHRNA protein for use in
CC  screening for candidate drugs to treat diseases related to CHRNA. The
CC  method of the invention is useful for haplotyping the CHRNA gene in an
CC  individual, and can also be used in pharmaceutical research to validate
CC  CHRNA as a candidate target for, and in design of clinical trials of
CC  candidate drugs for, treating a specific condition or disease
CC  predicted to be associated with CHRNA activity such as CMS. Polymorphisms
CC  in the target region may be determined by the use of allele-specific
CC  oligonucleotides (ASOs; ABL88370-ABL88320) as probes and primers, and by
CC  primer extension using oligonucleotide primers comprising sequences
CC  ABL88371-ABL88354. The CHRNA protein is useful for improving the
CC  efficiency and reliability of several steps in the discovery and
CC  development of drugs for treating diseases associated with CHRNA
CC  activity, and may be used to screen drugs which target CHRNA. Sequences
CC  ABL88287-ABL88320 represent specifically claimed allele-specific
CC  oligonucleotide (ASO) primers used for detecting polymorphisms in the
CC  CHRNA gene
XX
XX  Sequence 15 BP; 3 A; 6 C; 2 G; 3 T; 0 U; 1 Other;
SQ
Query Match      14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      33  GTCCTCTGAGAG 45
      :|:|||||

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Db      14 KTACTCTGAGAGG 2
RESULT 171
ABX01396/c
ID      AEX01396 standard; RNA; 15 BP.
XX
XX      AEX01396;
AC
XX      AEX01396;
AC
XX      23-DEC-2002 (first entry)
DT
XX
XX      Hepatitis C virus substrate #1178 for HCV hammerhead ribozyme #1178.
DE
XX
XX      Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW      HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW      liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW      type I interferon; interferon alpha; interferon beta; cytostatic;
KW      interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW      substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
XX      Hepatitis C virus.
OS
XX
XX      US2002082225-A1.
PN
XX
XX      27-JUN-2002.
PD
XX
XX      23-MAR-1999; 99US-00274553.
PF
XX
XX      23-MAR-1999; 99US-00274553.
PR
XX
XX      (BLAT/) BLATT L.
PA      (MCSW/) MCSWIGGEN J A.
PA      (ROBE/) ROBERTS B.
PA      (PAVC/) PAVCO P A.
PA      (MACE/) MACEJACK D.
XX
XX      Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
PI      WPI; 2002-617759/66.
XX
XX      New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT      replication and are useful to treat hepatitis C virus infections and
PT      cirrhosis, liver failure or hepatocellular carcinoma.
XX
XX      Claim 1; Page 55; 80pp; English.
PS
XX
XX      The present invention relates to enzymatic nucleic acids which
CC      specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC      enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC      (HP) motif where the binding arms comprise sequences complementary to one
CC      of the substrate sequences defined in the specification. The HCV
CC      ribozymes are useful for modulating the expression and/or replication of
CC      hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC      HCV. They can be used to treat cirrhosis, liver failure and/or
CC      hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC      a condition associated with HCV infection in conjunction with one or more
CC      other drug therapies, particularly type I interferon, especially
CC      interferon alpha, beta or gamma or consensus interferon. The present
CC      sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC      Some of the sequence data for this patent did not form part of the
CC      printed specification. The complete sequence data for this patent was
CC      obtained in electronic format directly from the USPTO web site at
CC      seqdata.uspto.gov/psipdIDEntry.html
XX
XX      Sequence 15 BP; 4 A; 3 C; 3 G; 0 T; 5 U; 0 Other;
SQ      Query Match 14.3%; Score 11; DB 1; Length 15;
      Best Local Similarity 100.0%; Pred. No. 1.2e+02;
      Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GTAAAGAGCCA 55
      |||||
Db      13 GTAAAGAGCCA 3

RESULT 173

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AEB76104/C
ID AEB76104 standard; RNA; 15 BP.
XX AC AEB76104;
XX DT 22-SEP-2005 (first entry)
XX DE Hepatitis C virus hammerhead ribozyme substrate sequence.
XX KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
XX KW antiviral; gene therapy; substrate; ss.
XX OS Hepatitis C virus.
XX PN US2002013458-A1.
XX PD 31-JAN-2002.
XX PP 15-FEB-2000; 2000US-00504231.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLATT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS E.
XX PA (PAVO/) PAVO P A.
XX PA (WACE/) WACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;
XX WPI; 2002-215899/27.
XX PT New enzymatic nucleic acid molecule, which specifically cleaves minus
XX strand RNA derived from hepatitis C virus, useful for modulating the
XX expression and/or replication of hepatitis C virus.
XX PS Example 1; Page 40; 65pp; English.
XX CC The invention relates to an enzymatic nucleic acid molecule which
XX specifically cleaves minus strand RNA derived from hepatitis C virus
XX (HCV). The binding arms of the molecule comprise ribozyme sequences. The
XX molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
XX Zinzyne motifs. Also described: (1) a pharmaceutical composition
XX comprising the novel enzymatic nucleic acid; (2) a mammalian cell
XX comprising a nucleic acid sequence encoding at least one enzymatic
XX nucleic acid molecule, in a manner, which allows expression of that
XX molecule; (4) a mammalian cell including an expression vector of (3); (5)
XX methods for treating cirrhosis, liver failure or hepatocellular carcinoma
XX by administering to a patient the novel enzymatic nucleic acid or the
XX associated with HCV infection, by contacting cells of the patient with
XX the nucleic acid molecule, and further employing one or more drug
XX therapies; (7) a method for inhibiting HCV replication in a mammalian
XX cell by administering the novel enzymatic nucleic acid; and (8) a method
XX of cleaving a separate RNA molecule by contacting the novel enzymatic
XX nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
XX is useful for modulating the expression and/or replication of hepatitis C
XX virus (HCV), and for inhibiting the expression of HCV minus strand. The
XX nucleic acid may also be used to treat or prevent the occurrence of a
XX disease state in a patient. The present sequence represents an HCV
XX hammerhead ribozyme target substrate sequence which is used in the
XX exemplification of the present invention.
XX SQ Sequence 15 BP; 4 A; 3 C; 3 G; 0 T; 5 U; 0 Other;
Query Match 14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 45 GTAAAGGCCA 55
Db 13 GTAAAGGCCA 3

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RESULT 174
AEB76105/C
ID AEB76105 standard; RNA; 15 BP.
XX AC AEB76105;
XX DT 22-SEP-2005 (first entry)
XX DE Hepatitis C virus hammerhead ribozyme substrate sequence.
XX KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
XX KW antiviral; gene therapy; substrate; ss.
XX OS Hepatitis C virus.
XX PN US2002013458-A1.
XX PD 31-JAN-2002.
XX PP 15-FEB-2000; 2000US-00504231.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLATT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS E.
XX PA (PAVO/) PAVO P A.
XX PA (WACE/) WACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;
XX WPI; 2002-215899/27.
XX PT New enzymatic nucleic acid molecule, which specifically cleaves minus
XX strand RNA derived from hepatitis C virus, useful for modulating the
XX expression and/or replication of hepatitis C virus.
XX PS Example 1; Page 40; 65pp; English.
XX CC The invention relates to an enzymatic nucleic acid molecule which
XX specifically cleaves minus strand RNA derived from hepatitis C virus
XX (HCV). The binding arms of the molecule comprise ribozyme sequences. The
XX molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
XX Zinzyne motifs. Also described: (1) a pharmaceutical composition
XX comprising the novel enzymatic nucleic acid; (2) a mammalian cell
XX comprising a nucleic acid sequence encoding at least one enzymatic
XX nucleic acid molecule, in a manner, which allows expression of that
XX molecule; (4) a mammalian cell including an expression vector of (3); (5)
XX methods for treating cirrhosis, liver failure or hepatocellular carcinoma
XX by administering to a patient the novel enzymatic nucleic acid or the
XX associated with HCV infection, by contacting cells of the patient with
XX the nucleic acid molecule, and further employing one or more drug
XX therapies; (7) a method for inhibiting HCV replication in a mammalian
XX cell by administering the novel enzymatic nucleic acid; and (8) a method
XX of cleaving a separate RNA molecule by contacting the novel enzymatic
XX nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
XX is useful for modulating the expression and/or replication of hepatitis C
XX virus (HCV), and for inhibiting the expression of HCV minus strand. The
XX nucleic acid may also be used to treat or prevent the occurrence of a
XX disease state in a patient. The present sequence represents an HCV
XX hammerhead ribozyme target substrate sequence which is used in the
XX exemplification of the present invention.
XX SQ Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```

Qy      45 GTAAAGAGCCA 55
Db      11 GTAAAGAGCCA 1

RESULT 175
AAT54540/c
ID      AAT54540 standard; RNA; 15 BP.
XX
AC      AAT54540;
XX
DT      25-MAR-2003 (revised)
DT      22-APR-1997 (first entry)
XX
DE      Mouse IL-5 hammerhead ribozyme target sequence (nt. position 36).
XX
KW      Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW      gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW      intercellular adhesion molecule; rel A; tumour necrosis factor;
KW      TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW      translocation; chronic myelogenous leukaemia; CML; cancer;
KW      Philadelphia chromosome; inflammation; autoimmune disease;
KW      atherosclerosis; myocardial infarction; stroke; restenosis;
KW      transplant rejection; rheumatoid arthritis; psoriasis;
KW      myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW      human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW      85.
XX
OS      Mus musculus.
XX
PN      WO9523225-A2.
XX
PD      31-AUG-1995.
XX
PF      23-FEB-1995; 95WO-IB000156.
XX
PR      23-FEB-1994; 94US-00201109.
PR      29-MAR-1994; 94US-00218934.
PR      04-APR-1994; 94US-00222795.
PR      07-APR-1994; 94US-00224483.
PR      15-APR-1994; 94US-00227958.
PR      18-MAY-1994; 94US-00228041.
PR      06-JUL-1994; 94US-00271280.
PR      15-AUG-1994; 94US-00291433.
PR      16-AUG-1994; 94US-00291433.
PR      17-AUG-1994; 94US-00292620.
PR      18-AUG-1994; 94US-00292620.
PR      19-AUG-1994; 94US-00293520.
PR      02-SEP-1994; 94US-00300000.
PR      08-SEP-1994; 94US-00303039.
PR      23-SEP-1994; 94US-00311486.
PR      28-SEP-1994; 94US-00314397.
PR      03-OCT-1994; 94US-00316771.
PR      07-OCT-1994; 94US-00319492.
PR      11-OCT-1994; 94US-00321993.
PR      04-NOV-1994; 94US-00334847.
PR      10-NOV-1994; 94US-00337608.
PR      28-NOV-1994; 94US-00345516.
PR      16-DEC-1994; 94US-00357577.
PR      23-DEC-1994; 94US-00363233.
PR      30-JAN-1995; 95US-00380734.
XX
PA      (RIBO-) RIBOZYME PHARM INC.
XX
PI      Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
PI      Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI      Modak A, Pavco P, Beigelman L, Sullivan SM, Sweedler D, Thompson JD;
PI      Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR      WPI; 1995-351090/45.
XX
XX      Ribozymes having modified bases and methods for producing them - for use
PT
in inhibiting disease related genes.
Claim 2; Page 220; 407pp; English.
The present sequence represents a preferred target sequence for an
enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-
5) mRNA at the nucleotide base position indicated in the DE line. Regions
of the mRNA that do not form secondary folding structures and that
contain potential hammerhead and hairpin ribozyme cleavage sites were
identified by computer analysis. Ribozymes directed against these mRNA
sequences were designed and synthesised with modifications that improve
their nuclease resistance. The ribozymes cleave the IL-5 target sequences
and thereby inhibit IL-5 expression, making them useful for treating
chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes
and preventing the recruitment and activation of eosinophils. The
ribozymes can also be used to treat eosinophilia (related to parasitic
infection or with pulmonary infiltration) and L-tryptophan-associated
eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
field.)
SQ      Sequence 15 BP; 5 A; 3 C; 4 G; 0 T; 3 U; 0 Other;
Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      25 ACTCTGGAGTCCTC 38
Db      14 ACTCTGAAGTCCTC 1
RESULT 176
AAT54538/c
ID      AAT54538 standard; RNA; 15 BP.
XX
AC      AAT54538;
XX
DT      25-MAR-2003 (revised)
DT      22-APR-1997 (first entry)
XX
DE      Mouse IL-5 hammerhead ribozyme target sequence (nt. position 36).
XX
KW      Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW      gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW      intercellular adhesion molecule; rel A; tumour necrosis factor;
KW      TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW      translocation; chronic myelogenous leukaemia; CML; cancer;
KW      Philadelphia chromosome; inflammation; autoimmune disease;
KW      atherosclerosis; myocardial infarction; stroke; restenosis;
KW      transplant rejection; rheumatoid arthritis; psoriasis;
KW      myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW      human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW      85.
XX
OS      Mus musculus.
XX
PN      WO9523225-A2.
XX
PD      31-AUG-1995.
XX
PF      23-FEB-1995; 95WO-IB000156.
XX
PR      23-FEB-1994; 94US-00201109.
PR      29-MAR-1994; 94US-00218934.
PR      04-APR-1994; 94US-00222795.
PR      07-APR-1994; 94US-00224483.
PR      15-APR-1994; 94US-00227958.
PR      18-MAY-1994; 94US-00228041.
PR      06-JUL-1994; 94US-00271280.
PR      15-AUG-1994; 94US-00291433.
PR      16-AUG-1994; 94US-00291433.
PR      17-AUG-1994; 94US-00292620.

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PR 19-AUG-1994; 94US-00293520.  
 PR 02-SEP-1994; 94US-00300000.  
 PR 08-SEP-1994; 94US-00303039.  
 PR 23-SEP-1994; 94US-00311486.  
 PR 23-SEP-1994; 94US-00311749.  
 PR 28-SEP-1994; 94US-00314397.  
 PR 03-OCT-1994; 94US-00316771.  
 PR 07-OCT-1994; 94US-00319492.  
 PR 11-OCT-1994; 94US-00321993.  
 PR 04-NOV-1994; 94US-00334847.  
 PR 10-NOV-1994; 94US-00337608.  
 PR 28-NOV-1994; 94US-00337608.  
 PR 16-DEC-1994; 94US-00335757.  
 PR 23-DEC-1994; 94US-00363233.  
 PR 30-JAN-1995; 95US-00380734.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Stinchcomb DT, Chowrira B, Dizenzo A, Draper KG, Dudycz LW;  
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Ueman N, Wincott FR, Woolf T;  
 XX  
 XX WPI; 1995-351090/45.  
 XX  
 XX Ribozyms having modified bases and methods for producing them - for use  
 XX in inhibiting disease related genes.  
 XX  
 XX Claim 2; Page 220; 407pp; English.  
 XX  
 CC The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-  
 CC 5) mRNA at the nucleotide base position indicated in the DE line. Regions  
 CC of the mRNA that do not form secondary folding structures and that  
 CC contain potential hammerhead and hairpin ribozyme cleavage sites were  
 CC identified by computer analysis. Ribozymes directed against these mRNA  
 CC sequences were designed and synthesised with modifications that improve  
 CC their nuclease resistance. The ribozymes cleave the IL-5 target sequences  
 CC and thereby inhibit IL-5 expression, making them useful for treating  
 CC chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes  
 CC and preventing the recruitment and activation of eosinophils. The  
 CC ribozymes can also be used to treat eosinophilia (related to parasitic  
 CC infection or with pulmonary infiltration) and L-tryptophan-associated  
 CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI  
 CC field.)  
 XX  
 XX Sequence 15 BP; 5 A; 3 C; 4 G; 0 T; 3 U; 0 Other;  
 XX  
 SQ Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 25 ACTCTGGAGTCCTC 38  
 Db ||||| |||||  
 14 ACTCTGAAGTCCTC 1  
 RESULT 177  
 AAT55140  
 ID AAT55140 standard; RNA; 15 BP.  
 XX  
 AC AAT55140;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 21-APR-1997 (first entry)  
 XX  
 XX Human relA hammerhead ribozyme target sequence (nt. position 1566).  
 DE  
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW Gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
 KW translocation; chronic myelogenous leukaemia; CML; cancer;  
 KW

KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 XX 88.  
 OS Homo sapiens.  
 XX  
 XX W09523225-A2.  
 XX  
 PD 31-AUG-1995.  
 XX  
 PF 23-FEB-1995; 95WO-IB000156.  
 XX  
 PR 23-FEB-1994; 94US-00201109.  
 PR 29-MAR-1994; 94US-00218934.  
 PR 04-APR-1994; 94US-00222795.  
 PR 07-APR-1994; 94US-00224483.  
 PR 15-APR-1994; 94US-00227958.  
 PR 15-APR-1994; 94US-00228041.  
 PR 18-MAY-1994; 94US-00245736.  
 PR 06-JUL-1994; 94US-00271280.  
 PR 15-AUG-1994; 94US-00291322.  
 PR 16-AUG-1994; 94US-00291433.  
 PR 17-AUG-1994; 94US-00292620.  
 PR 19-AUG-1994; 94US-00293520.  
 PR 02-SEP-1994; 94US-00300000.  
 PR 08-SEP-1994; 94US-00303039.  
 PR 23-SEP-1994; 94US-00311486.  
 PR 23-SEP-1994; 94US-00311749.  
 PR 28-SEP-1994; 94US-00314397.  
 PR 03-OCT-1994; 94US-00316771.  
 PR 07-OCT-1994; 94US-00319492.  
 PR 11-OCT-1994; 94US-00321993.  
 PR 04-NOV-1994; 94US-00334847.  
 PR 10-NOV-1994; 94US-00337608.  
 PR 28-NOV-1994; 94US-00345516.  
 PR 16-DEC-1994; 94US-00357577.  
 PR 23-DEC-1994; 94US-00363233.  
 PR 30-JAN-1995; 95US-00380734.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Stinchcomb DT, Chowrira B, Dizenzo A, Draper KG, Dudycz LW;  
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Ueman N, Wincott FR, Woolf T;  
 XX  
 XX WPI; 1995-351090/45.  
 XX  
 XX Ribozyms having modified bases and methods for producing them - for use  
 XX in inhibiting disease related genes.  
 XX  
 XX Claim 2; Page 229; 407pp; English.  
 XX  
 CC The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the  
 CC nucleotide base position indicated in the DE line. The relA gene product  
 CC is a subunit of the transcriptional regulator NF-kappaB and is implicated  
 CC specifically in the induction of inflammatory responses. Regions of the  
 CC mRNA that do not form secondary folding structures and that contain  
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified  
 CC by computer analysis. Ribozymes directed against these mRNA sequences  
 CC were designed and synthesised with modifications that improve their  
 CC nuclease resistance. The ribozymes are designed to cleave the target  
 CC sequences and thereby inhibit relA expression, making them potentially  
 CC useful for treating rheumatoid arthritis, restenosis and asthma as well  
 CC as for increasing tolerance to transplanted tissues. The potential  
 CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means  
 CC that uses are limited to local delivery, acute indications or ex vivo  
 CC treatment. (Updated on 25-MAR-2003 to correct PI field.)  
 XX

SQ Sequence 15 BP; 4 A; 3 C; 5 G; 0 T; 3 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 64.3%; Pred. No. 1.3e+02;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTGAG 42  
 :|||:|:|:|:  
 Db 2 UGGAGUACCCUGAG 15

RESULT 178  
 AAZ62575/c  
 ID AAZ62575 standard; RNA; 15 BP.  
 AC AAZ62575;  
 XX  
 DT 28-MAR-2000 (first entry)  
 XX  
 DE Substrate for HH ribozyme HCV-3329 which cleaves HCV RNA at nt. 3329.  
 XX  
 DE Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;  
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;  
 KW autoimmune disease; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN W09955847-A2.  
 XX  
 PI 04-NOV-1999.  
 XX  
 XX 26-APR-1999; 99WO-US009027.  
 XX  
 PR 27-APR-1998; 98US-0083217P.  
 PR 18-SEP-1998; 98US-0100842P.  
 PR 25-FEB-1999; 99US-00257608.  
 PR 23-MAR-1999; 99US-00274553.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Blatt L, Meswigen JA, Roberts E, Pavco PA, Macejak D;  
 XX WPI; 2000-062023/05.  
 XX  
 XX Novel ribozymes for the treatment of diseases and conditions related to  
 PT hepatitis C infection.  
 XX  
 PS Claim 1; Page 56; 123pp; English.  
 XX  
 CC The present sequence represents the preferred target sequence of an  
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in  
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme  
 CC target sites using a computer folding algorithm and regions of the mRNA  
 CC which did not form secondary folding structures and contained potential  
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to  
 CC target these sites and their activities optimised by either varying the  
 CC length of the binding arms or by modification to prevent degradation by  
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or  
 CC viral replication, and are used to treat diseases associated with  
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and  
 CC hepatocellular carcinoma. The ribozymes may be used in combination with  
 CC interferon to treat HCV infection, other infectious diseases, autoimmune  
 CC diseases, and cancer  
 XX  
 SQ Sequence 15 BP; 3 A; 3 C; 5 G; 0 T; 4 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGTCC 70  
 | ||| |||||

Db 15 CCAAGATGATGTCC 2

RESULT 179  
 AAZ90853  
 ID AAZ90853 standard; DNA; 15 BP.  
 XX  
 AC AAZ90853;  
 XX  
 DT 24-MAY-2000 (first entry)  
 XX  
 DE Human NR8 gene probe #81.  
 XX  
 KW Haemopoietin receptor family; NR8; antibody; diagnosis;  
 KW blood formation disorder; fusion protein; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09967290-A1.  
 XX  
 PD 29-DEC-1999.  
 XX  
 PF 23-JUN-1999; 99WO-JP003351.  
 XX  
 PR 24-JUN-1998; 98JP-00214720.  
 PR 19-OCT-1998; 98JP-00297409.  
 XX  
 XX (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.  
 XX  
 PI Nomura H, Maeda M;  
 XX  
 DR WPI; 2000-116933/10.  
 XX  
 XX Hemopoietin receptor protein family NR8 used for diagnosis of blood  
 PT formation disorders.  
 XX  
 PS Example 1; Page 41; 176pp; Japanese.  
 XX  
 CC The invention relates to the isolation of sequences encoding human  
 CC haemopoietin receptor protein family NR8 genes. The NR8 family sequences  
 CC were initially searched for comparison on a nucleic acid database with  
 CC the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid  
 CC sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ9258-259300 and AAZ90816-  
 CC Z90925 represent specific examples of probe sequences used in the search.  
 CC Antibodies to the NR8 family proteins are used for the diagnosis of blood  
 CC formation disorders. Compounds identified as binding to the proteins are  
 CC used for the treatment of such disorders  
 XX  
 SQ Sequence 15 BP; 2 A; 3 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTGAG 42  
 :|||:|:|:|:  
 Db 1 TGGAGTCCTTGGAG 14

RESULT 180  
 AAA63392/c  
 ID AAA63392 standard; DNA; 15 BP.  
 XX  
 AC AAA63392;  
 XX  
 DT 06-MAR-2001 (first entry)  
 XX  
 DE C-1027 gene cluster reverse PCR primer for ORF 12.  
 XX  
 KW Eneidyne C-1027 biosynthesis gene cluster; apoprotein; chromophore;  
 KW PCR primer; ss.  
 XX  
 OS Streptomyces globisporus.

XX WO200040596-A1.  
 XX 13-JUL-2000.  
 XX 06-JAN-2000; 2000WO-US000446.  
 XX 06-JAN-1999; 99US-0115434P.  
 XX 05-JAN-2000; 2000US-00477962.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX  
 XX Shen B, Liu W, Christenson SD, Standage S;  
 XX WPI; 2000-465947/40.  
 XX  
 XX Isolated nucleic acid comprising a nucleic acid encoding any of C-1027  
 XX open reading frames (ORFs) -7 to 42, excluding ORF 9 (caga), useful for  
 XX the production of enedyme C-1027 antitumor antibiotics.  
 XX  
 XX Disclosure; Page 17; 160pp; English.  
 XX  
 XX The present invention is concerned with the elucidation of the gene  
 XX cluster from Streptomyces globisporus which regulates enedyme C-1027  
 XX synthesis. Enedyme C-1027 is an antibiotic, consisting of an apoprotein  
 XX and a non-peptidic chromophore, which causes damage to DNA. The primers  
 XX AAA63353-A63451 were used to isolate the open reading frames which  
 XX comprise the gene cluster. The sequences within the gene cluster can be  
 XX used to produce the protein and to identify antagonists, both of which  
 XX can be used in the treatment of cancer  
 XX  
 XX Sequence 15 BP; 3 A; 3 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 AACCAAGACGCGCTG 16  
 Db 15 AACCAAGTCGTCCTG 2  
 ||||| |||||  
 RESULT 181  
 AAF49814  
 ID AAF49814 standard; DNA; 15 BP.  
 XX  
 XX AC AAF49814;  
 XX  
 XX 30-MAR-2001 (first entry)  
 XX IGF-I oligonucleotide #774.  
 XX  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 XX hyperneovascular condition; hyperplasia; kidney disease;  
 XX neovascular condition of the retina; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200078341-A1.  
 XX 28-DEC-2000.  
 XX  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX 21-JUN-1999; 99US-0140345P.  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 XX Wraith CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.

PI Wraith CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 XX inhibits or reduces growth factor mediated cell proliferation and/or  
 XX inflammation.  
 XX  
 XX Example 8; Page 65; 201pp; English.  
 XX  
 XX The present invention relates to a method for ameliorating the effects of  
 XX skin disorders. The method comprises contacting the skin with an  
 XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 XX inhibiting or reducing growth factor mediated cell proliferation,  
 XX inflammation and/or other disorders. The present sequence is an  
 XX oligonucleotide which can be used to design the antisense  
 XX oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 XX P45161). The method is useful for ameliorating the effects of psoriasis,  
 XX ichthyosis, scleroderma, warts, benign growths, cancers of the skin, a  
 XX neoplasias, pilaris, pilaris, pilaris, serborrhea, keloids, keratosis,  
 XX hyperneovascular condition such as a neovascular condition of the retina,  
 XX brain or skin, growth factor-mediated malignancies, other sclerotic  
 XX diseases, kidney disease, hyperproliferation of the inside of blood  
 XX vessels or any other hyperplasia  
 XX  
 XX Sequence 15 BP; 4 A; 6 C; 4 G; 1 T; 0 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 AACCAAGACGCGCTG 16  
 Db 2 AACGACACGCGCTG 15  
 ||||| |||||  
 RESULT 182  
 AAF52685  
 ID AAF52685 standard; DNA; 15 BP.  
 XX  
 XX AC AAF52685;  
 XX  
 XX 30-MAR-2001 (first entry)  
 XX IGF-I oligonucleotide #3645.  
 XX  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 XX hyperneovascular condition; hyperplasia; kidney disease;  
 XX neovascular condition of the retina; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200078341-A1.  
 XX 28-DEC-2000.  
 XX  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX 21-JUN-1999; 99US-0140345P.  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 XX Wraith CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.

XX Example 8; Page 84; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 33 GTCTCTGAGAGGT 46  
 |||||  
 Db 2 GTCTCTGGGAGAT 15

RESULT 183  
 AAF49815  
 ID AAF49815 standard; DNA; 15 BP.

AC AAF49815;

XX 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #775.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.

XX Example 8; Page 66; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 4 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AACACAGACGCCCTG 16  
 |||||  
 Db 1 AACGACACGCCCTG 14

RESULT 184  
 AAF46719/c  
 ID AAF46719 standard; DNA; 15 BP.

XX AAF46719;

XX 30-MAR-2001 (first entry)

DE IGFBP3 oligonucleotide #139.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.

XX Example 7; Page 45; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 AGAGCCAGCGAAGC 62  
 Db ||||| ||||| |||||  
 15 AGAGTCAGCGCAGC 2

RESULT 185  
 AAF46720/c  
 ID AAF46720 standard; DNA; 15 BP.  
 XX AC AAF46720;  
 XX DT 30-MAR-2001 (first entry)  
 XX DB IGFBP3 oligonucleotide #140.  
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX OS Homo sapiens.  
 XX PN WO200078341-A1.  
 XX PD 28-DEC-2000.  
 XX PF 21-JUN-2000; 2000WO-AU000693.  
 XX PR 21-JUN-1999; 99US-0140345P.  
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX PI Wraight CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 XX inhibits or reduces growth factor mediated cell proliferation and/or  
 XX inflammation.  
 XX PS Example 7; Page 45; 201pp; English.  
 XX CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia

CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 1 A; 5 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 AGAGCCAGCGAAGC 62  
 Db ||||| ||||| |||||  
 14 AGAGTCAGCGCAGC 1

RESULT 186  
 AAF52027  
 ID AAF52027 standard; DNA; 15 BP.  
 XX AC AAF52027;  
 XX DT 30-MAR-2001 (first entry)  
 XX DB IGF-I oligonucleotide #2987.  
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX OS Homo sapiens.  
 XX PN WO200078341-A1.  
 XX PD 28-DEC-2000.  
 XX PF 21-JUN-2000; 2000WO-AU000693.  
 XX PR 21-JUN-1999; 99US-0140345P.  
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX PI Wraight CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 XX inhibits or reduces growth factor mediated cell proliferation and/or  
 XX inflammation.  
 XX PS Example 8; Page 80; 201pp; English.  
 XX CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia

CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 54 CAGCGAGCTGATG 67  
 DB 2 CAGCGCTGCTGATG 15  
 ||||| |||||  
 ||||| |||||

RESULT 187  
 AAF52686  
 ID AAF52686 standard; DNA; 15 BP.  
 XX  
 AC AAF52686;  
 XX  
 DT 30-MAR-2001 (first entry)  
 XX  
 DE IGF-I oligonucleotide #3646.  
 XX  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WQ200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wraight CJ, Werther GA, Edmondson SR;  
 XX  
 DR WPI; 2001-041421/05.  
 XX  
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 8; Page 84; 20pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 33 GTCCTCTGAGGCT 46  
 DB 1 GTCCTCTGGGAGAT 14  
 ||||| |||||  
 ||||| |||||

RESULT 188  
 AAF50644/C  
 ID AAF50644 standard; DNA; 15 BP.  
 XX  
 AC AAF50644;  
 XX  
 DT 30-MAR-2001 (first entry)  
 XX  
 DE IGF-I oligonucleotide #1604.  
 XX  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WQ200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wraight CJ, Werther GA, Edmondson SR;  
 XX  
 DR WPI; 2001-041421/05.  
 XX  
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 8; Page 71; 20pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 3 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 54 CAGCGAAGCTGATG 67  
 DB 15 CGGTGAAGCTGATG 2

## RESULT 189

AAF52029

ID AAF52029 standard; DNA; 15 BP.

XX

AC AAF52029;

XX

DT 30-MAR-2001 (first entry)

XX

DB IGF-I oligonucleotide #2989.

XX

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 hyperneovascular condition; hyperplasia; kidney disease;  
 neovascular condition of the retina; ss.

XX

OS Homo sapiens.

XX

PN WO200078341-A1.

XX

PD 28-DEC-2000.

XX

PF 21-JUN-2000; 2000WO-AU000693.

XX

PR 21-JUN-1999; 99US-0140345P.

XX

PA (MURD-) MURDOCH CHILDRENS RES INST.

XX

PI Wright CJ, Werther GA, Edmondson SR;

XX

DR WPI; 2001-041421/05.

XX

Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 inhibits or reduces growth factor mediated cell proliferation and/or  
 inflammation.

XX

PS Example 8; Page 80; 201pp; English.

XX

The present invention relates to a method for ameliorating the effects of  
 skin disorders. The method comprises contacting the skin with an  
 antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 inhibiting or reducing growth factor mediated cell proliferation,  
 inflammation and/or other disorders. The present sequence is an  
 oligonucleotide which can be used to design the antisense  
 oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 F45161). The method is useful for ameliorating the effects of psoriasis,  
 ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 hyperneovascular condition such as a neovascular condition of the retina,  
 brain or skin, growth factor-mediated malignancies, other sclerotic  
 disease, kidney disease, hyperproliferation of the inside of blood  
 vessels or any other hyperplasia

XX

SQ Sequence 15 BP; 2 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

## Query Match

14.0%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGT 68

DB 1 AGCGTCTGCTGATGT 14

## RESULT 190

AAF50645/C

ID AAF50645 standard; DNA; 15 BP.

XX

AC AAF50645;

XX

DT 30-MAR-2001 (first entry)

XX

DB IGF-I oligonucleotide #1605.

XX

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 hyperneovascular condition; hyperplasia; kidney disease;  
 neovascular condition of the retina; ss.

XX

OS Homo sapiens.

XX

PN WO200078341-A1.

XX

PD 28-DEC-2000.

XX

PF 21-JUN-2000; 2000WO-AU000693.

XX

PR 21-JUN-1999; 99US-0140345P.

XX

PA (MURD-) MURDOCH CHILDRENS RES INST.

XX

PI Wright CJ, Werther GA, Edmondson SR;

XX

DR WPI; 2001-041421/05.

XX

Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 inhibits or reduces growth factor mediated cell proliferation and/or  
 inflammation.

XX

PS Example 8; Page 71; 201pp; English.

XX

The present invention relates to a method for ameliorating the effects of  
 skin disorders. The method comprises contacting the skin with an  
 antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 inhibiting or reducing growth factor mediated cell proliferation,  
 inflammation and/or other disorders. The present sequence is an  
 oligonucleotide which can be used to design the antisense  
 oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 F45161). The method is useful for ameliorating the effects of psoriasis,  
 ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 hyperneovascular condition such as a neovascular condition of the retina,  
 brain or skin, growth factor-mediated malignancies, other sclerotic  
 disease, kidney disease, hyperproliferation of the inside of blood  
 vessels or any other hyperplasia

XX

SQ Sequence 15 BP; 3 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

## Query Match

14.0%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 54 CAGCGAAGCTGATG 67

DB 14 CGGTGAAGCTGATG 1



RESULT 191  
ADV37122/c  
ID ADV37122 standard; RNA; 15 BP.  
XX  
AC ADV37122;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human anti-HER2 NCH ribozyme substrate sequence #954.  
XX  
KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTPB-1B; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200116312-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000WO-US023998.  
XX  
PR 31-AUG-1999; 99US-0151713P.  
PR 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 27-SEP-1999; 99US-0156236P.  
PR 08-NOV-1999; 99US-00436430.  
PR 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
PR 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
PI Karpaisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX  
DR WPI; 2001-244406/25.  
XX  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
PT obesity and heart disease.  
XX  
PS Example 7; Page 491; 717pp; English.  
XX  
XX The present invention relates to the use of enzymatic nucleic acid  
XX molecules (e.g. ribozymes) to modulate gene expression. The invention of  
XX also methods for their use to down regulate or inhibit the expression of  
XX genes encoding protein-tyrosine-phosphatase-1b (PTP-1B), methionine  
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
XX receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
XX nucleic acid molecules used to inhibit the expression of the said genes  
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,  
XX zinzyme, and/or DNazyme motifs. The methods of the invention are useful  
XX for treating cancer, in particular breast cancer, Alzheimer's disease,  
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related

CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
CC diagnostic tools to examine genetic drift and mutations within diseased  
CC cells and to detect the presence of specific RNA in a cell. The present  
CC sequence represents a substrate/target sequence for an anti-HER2 NCH  
CC ribozyme used in the examples of the present invention. Note: Some SEQ ID  
CC Nos are repeated more than once in the specification, but these have  
CC different sequences associated with them.  
XX  
SQ Sequence 15 BP; 5 A; 5 C; 4 G; 0 T; 1 U; 0 Other;  
Query Match 14.0%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. NO. 1.3e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 25 ACTCTGGAGTCTTC 38  
Db 14 ACTGTGGGGTCTTC 1  
RESULT 192  
ADV35537/c  
ID ADV35537 standard; RNA; 15 BP.  
XX  
AC ADV35537;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human anti-HER2 NCH ribozyme substrate sequence #168.  
XX  
KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTPB-1B; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200116312-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000WO-US023998.  
XX  
PR 31-AUG-1999; 99US-0151713P.  
PR 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 27-SEP-1999; 99US-0156236P.  
PR 08-NOV-1999; 99US-00436430.  
PR 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
PR 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
PI Karpaisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX  
DR WPI; 2001-244406/25.  
XX  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
PT



are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

Example 7; Page 474; 717pp; English.

The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention of also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for an anti-HER2 NCH ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.

Sequence 15 BP; 1 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 ACGGCTGGGGGATA 22  
||||| |||||  
Db 15 ACGGCTAGGGGATA 2

RESULT 193

ADV37121/c  
ID ADV37121 standard; RNA; 15 BP.

AC ADV37121;

XX 10-FEB-2005 (first entry)

XX Human anti-HER2 NCH ribozyme substrate sequence #953.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberzyme; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
ss.

XX Homo sapiens.

XX WO200116312-A2.

XX 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US023398.

XX 31-AUG-1999; 99US-0151713P.

XX 27-SEP-1999; 99US-00406643.

XX 27-SEP-1999; 99US-0156236P.

XX 27-SEP-1999; 99US-0156457P.

XX 08-NOV-1999; 99US-00436430.

XX 06-DEC-1999; 99US-0169100P.

PR 29-DEC-1999; 99US-00474432.  
PR 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.

XX Mcswiggen J, Ueman N, Blatt L, Beigelman L, Burgin A;  
XX Karpelsky A, Matulic-Adamic J, Svedler D, Draper K, Chowrira B;  
XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

Example 7; Page 491; 717pp; English.

The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention of also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for an anti-HER2 NCH ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.

Sequence 15 BP; 4 A; 5 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 25 ACTCTGGAGTCTC 38  
||| ||| ||| |||  
Db 15 ACTGTGGGTCTC 2

RESULT 194

ADV35538/c

ID ADV35538 standard; RNA; 15 BP.

XX ADV35538;

XX 10-FEB-2005 (first entry)

XX Human anti-HER2 NCH ribozyme substrate sequence #169.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberzyme; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;

KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
 KW ss.

XX Homo sapiens.

XX WO200116312-A2.

XX 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US023998.

XX 31-AUG-1999; 99US-0151713P.

XX 27-SEP-1999; 99US-00406643.

XX 27-SEP-1999; 99US-0156236P.

XX 27-SEP-1999; 99US-0156467P.

XX 08-NOV-1999; 99US-00436430.

XX 06-DEC-1999; 99US-0169100P.

XX 29-DEC-1999; 99US-00474432.

XX 30-DEC-1999; 99US-00476387.

XX 04-FEB-2000; 2000US-00498824.

XX 20-MAR-2000; 2000US-00531025.

XX 14-APR-2000; 2000US-0197769P.

XX 23-MAY-2000; 2000US-00578223.

XX 09-AUG-2000; 2000US-00636385.

XX (RIBO-) RIBOZYME PHARM INC.

XX McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
 PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
 XX WPI; 2001-244406/25.

XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
 PT obesity and heart disease.

XX Example 7; Page 474; 717pp; English.

XX The present invention relates to the use of enzymatic nucleic acid  
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
 CC also methods for their use to down regulate or inhibit the expression of  
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
 CC aminopeptidase (MeCAP-2), human telomerase (hTERT), protein kinase C  
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 CC nucleic acid molecules used to inhibit the expression of the said genes  
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
 CC zincyme, and/or DNAzyme motifs. The methods of the invention are useful  
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinomas. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a substrate/target sequence for an anti-HER2 NCH  
 CC ribozyme used in the examples of the present invention. Note: Some SEQ ID  
 CC Nos are repeated more than once in the specification, but these have  
 CC different sequences associated with them.

XX Sequence 15 BP; 1 A; 5 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 ACGGCTGGGGATA 22

DB 14 ACGGCCAGGGCATA 1

RESULT 195

ABK97479

ID ABK97479 standard; DNA; 15 BP.

XX AC ABK97479;

XX 07-OCT-2002 (first entry)

XX Human LCAT gene polymorphism detection ASO probe #2.

XX Lecithin-cholesterol acyltransferase; LCAT; Norum disease; gene therapy;  
 KW fish-eye disease; atherosclerotic cardiovascular disease; forensic;  
 KW population diversity; anthropological lineage; paternity testing; human;  
 KW polymorphism; allele-specific oligonucleotide; ASO; probe; ss.

XX Homo sapiens.

XX WO200253575-A1.

XX 11-JUL-2002.

XX 03-JAN-2001; 2001WO-US000092.

XX 03-JAN-2001; 2001WO-US000092.

XX (GENA-) GENAISANCE PHARM INC.

XX Chew A, Denton RR, Nandabalan K, Stephens JC;  
 PI WPI; 2002-557737/59.

XX Novel isolated polymorphic variant polynucleotide of lecithin-cholesterol  
 PT acyltransferase gene, useful for studying expression and biological  
 PT function of the gene, and for therapeutic, diagnostic or forensic  
 PT purposes.

XX Claim 16; Page 16; 72pp; English.

XX The present invention relates to a new polynucleotide comprising a  
 CC nucleotide sequence which is a polymorphic variant of a reference  
 CC sequence for lecithin-cholesterol acyltransferase (LCAT). The invention  
 CC is useful for identifying an association between a trait (preferably a  
 CC clinical response to drug targeting LCAT) and at least one genotype or  
 CC haplotype of LCAT gene. The method of the invention has applicability in  
 CC developing diagnostic tests and therapeutic treatments for Norum disease,  
 CC fish-eye disease and atherosclerotic cardiovascular disease. The  
 CC haplotyping and genotyping methods are useful for studying population  
 CC diversity, anthropological lineage, the significance of diversity and  
 CC lineage at the phenotypic level, paternity testing, forensic applications  
 CC and for identifying association between the LCAT genetic variation and a  
 CC trait such as level of drug response or susceptibility to disease. In  
 CC addition, the methods for identifying the LCAT haplotypes present in  
 CC individuals are useful in the development of drugs targeting LCAT. For  
 CC example, determining the frequency of individual LCAT haplotypes in a  
 CC population with a specific disease, e.g. Norum disease, will facilitate  
 CC the development of drugs targeting the LCAT isoform(s) that are most  
 CC frequent in that disease population. The present nucleic acid sequence  
 CC represents one of a collection (ABK97478-ABK97491) of allele-specific  
 CC oligonucleotide (ASO) probes that were used in the invention to detect  
 CC polymorphisms in the human LCAT gene

XX Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 52 GCCAGCGAGAGCTGA 65

DB 1 GACAGCTTAGCTGA 14

RESULT 196  
 AAS99164/C  
 ID AAS99164 standard; DNA; 15 BP.  
 XX  
 AC AAS99164;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE UDP glycosyltransferase 1 (UGT1A1) allele-specific oligonucleotide #31.  
 XX  
 KW UDP glycosyltransferase 1; UGT1A1; human; haplotyping; ss;  
 KW drug discovery; Gilbert's syndrome; Crigler-Najjar syndrome;  
 KW allele-specific oligonucleotide.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200179230-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 13-APR-2001; 2001WO-US012273.  
 XX  
 PR 18-APR-2000; 2000US-0197514P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Chew A, Choi JY, Koshy B, Rounds E;  
 XX  
 DR WPI; 2002-075063/10.  
 XX  
 XX Genotyping a human UDP glycosyltransferase 1 gene of an individual for  
 PT determining the haplotype of an individual, involves determining the  
 PT identity of a nucleotide pair at specific polymorphic sites for two  
 PT copies of the gene.  
 XX  
 PS Claim 16; Page 13; 81pp; English.  
 XX  
 CC The invention relates to genotyping a human UDP glycosyltransferase  
 CC (UGT1A1) gene of an individual, involving determining for the two copies  
 CC of the UGT1A1 gene present in the individual, the identity of the  
 CC nucleotide pair at one or more polymorphic sites. The new method is  
 CC useful for determining whether an individual has a haplotype or haplotype  
 CC pairs, given in the specification. It is useful for improving the  
 CC efficacy and reliability of several steps in the discovery and  
 CC development of drugs for treating diseases associated with UGT1A1  
 CC activity, e.g., Gilbert's syndrome and Crigler-Najjar syndrome, to  
 CC validate UGT1A1 as a candidate agent for treating a specific condition or  
 CC disease predicted to be associated with UGT1A1 activity, and in the  
 CC design of clinical trials of candidate drugs for treating a specific  
 CC condition or disease predicted to be associated with UGT1A1 activity. The  
 CC method is useful to screen for compounds targeting UGT1A1 to treat a  
 CC specific condition or disease associated with UGT1A1 activity. A nucleic  
 CC acid (I) comprising a polymorphic variant of a reference sequence for the  
 CC UGT1A1 gene or cDNA (II) or its fragment is useful in studying the  
 CC expression and function of UGT1A1, and in expressing UGT1A1 protein for  
 CC use in screening for candidate drugs to treat diseases related to UGT1A1  
 CC activity. (I) or (II) is useful for therapeutic purposes. (II) or a  
 CC recombinant organism comprising (II) is useful for studying expression of  
 CC the UGT1A1 isogenes in vivo, for in vivo screening and testing of drugs  
 CC targeted against UGT1A1 protein, and for testing the efficacy of  
 CC therapeutic agents and compounds for Gilbert's syndrome and Crigler-  
 CC Najjar syndrome, in a biological system. AAS99134-AAS99203 represent UDP  
 CC glycosyltransferase 1 gene allele-specific oligonucleotides used in the  
 CC method of the invention  
 XX  
 SQ Sequence 15 BP; 3 A; 5 C; 4 G; 2 T; 0 U; 1 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 28 CTGAGTCTCTCTGA 41  
 ||| |||||

Db 15 CRGGGGTCTCTGA 2  
 RESULT 197  
 ABX00426/c  
 ID ABX00426 standard; RNA; 15 BP.  
 XX  
 AC ABX00426;  
 XX  
 DT 23-DEC-2002 (first entry)  
 XX  
 DE Hepatitis C virus substrate #208 for HCV hammerhead ribozyme #208.  
 XX  
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
 KW type I interferon; interferon alpha; interferon beta; cytostatic;  
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;  
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US2002082225-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 23-MAR-1999; 99US-00274553.  
 XX  
 PR 23-MAR-1999; 99US-00274553.  
 XX  
 XX (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (ROBE/) ROBERTS B.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;  
 XX  
 DR WPI; 2002-617759/66.  
 XX  
 XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral  
 PT replication and are useful to treat hepatitis C virus infections and  
 PT cirrhosis, liver failure or hepatocellular carcinoma.  
 XX  
 PS Claim 1; Page 27; 80pp; English.  
 XX  
 CC The present invention relates to enzymatic nucleic acids which  
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin  
 CC (HP) motif where the binding arms comprise sequences complementary to one  
 CC of the substrate sequences defined in the specification. The HCV  
 CC ribozymes are useful for modulating the expression and/or replication of  
 CC HCV. They can be used to treat cirrhosis, liver failure and/or  
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating  
 CC a condition associated with HCV infection in conjunction with one or more  
 CC other drug therapies, particularly type I interferon, especially  
 CC interferon alpha, beta or gamma or consensus interferon. The present  
 CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:  
 CC Some of the sequence data for this patent did not form part of the  
 CC printed specification. The complete sequence data for this patent was  
 CC obtained in electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/patpsdIDEntry.html  
 XX  
 SQ Sequence 15 BP; 3 A; 3 C; 5 G; 0 T; 4 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 57 CGAAGCTGATGTC 70  
 ||| |||||

Db 15 CCAGATGATGTC 2

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RESULT 198
ADB74336/C
ID AEB74336 standard; RNA; 15 BP.
XX AC AEB74336;
XX AC
XX DT 22-SEP-2005 (first entry)
XX DE Hepatitis C virus hammerhead ribozyme substrate sequence.
XX ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
XX antiviral; gene therapy; substrate; ss.
XX KW Hepatitis C virus.
XX OS
XX PN US202013458-A1.
XX PD 31-JAN-2002.
XX PF 15-FEB-2000; 2000US-00504231.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS E.
XX PA (PAVO/) PAVO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;
XX WPI; 2002-215899/27.
XX DR
XX PT New enzymatic nucleic acid molecule, which specifically cleaves minus
XX strand RNA derived from hepatitis C virus, useful for modulating the
XX expression and/or replication of hepatitis C virus.
XX Example 1; Page 26; 65pp; English.
XX The invention relates to an enzymatic nucleic acid molecule which
XX specifically cleaves minus strand RNA derived from hepatitis C virus
XX (HCV). The binding arms of the molecule comprise ribozyme sequences. The
XX molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
XX Zinzyne motifs. Also described: (1) a pharmaceutical composition,
XX comprising the novel enzymatic nucleic acid; (2) a mammalian cell
XX including the novel enzymatic nucleic acid; (3) an expression vector
XX comprising a nucleic acid sequence encoding at least one enzymatic
XX nucleic acid molecule, in a manner, which allows expression of that
XX molecule; (4) a mammalian cell including an expression vector of (3); (5)
XX methods for treating cirrhosis, liver failure or hepatocellular carcinoma
XX by administering to a patient the novel enzymatic nucleic acid or the
XX vector of (3); (6) a method of treating a patient having a condition
XX associated with HCV infection, by contacting cells of the patient with
XX the nucleic acid molecule, and further employing one or more drug
XX therapies; (7) a method for inhibiting HCV replication in a mammalian
XX cell by administering the novel enzymatic nucleic acid; and (8) a method
XX of cleaving a separate RNA molecule by contacting the novel enzymatic
XX nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
XX is useful for modulating the expression and/or replication of hepatitis C
XX virus (HCV), and for inhibiting the expression of HCV minus strand. The
XX nucleic acid may also be used to treat or prevent the occurrence of a
XX disease state in a patient. The present sequence represents an HCV
XX hammerhead ribozyme target substrate sequence which is used in the
XX exemplification of the present invention.
XX SQ Sequence 15 BP; 3 A; 3 C; 5 G; 0 T; 4 U; 0 Other;
Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 57 CGAAGCTGATGTC 70

RESULT 199
ADP47133
ID ADP47133 standard; DNA; 15 BP.
XX AC ADP47133;
XX AC
XX DT 09-SEP-2004 (first entry)
XX DE Human phospholipase A2-specific mAb heavy chain DNA sequence #13.
XX human; monoclonal antibody; phospholipase A2; PLA2;
XX inflammatory disorder; degenerative disorder;
XX joint inflammatory reaction; skin inflammatory reaction;
XX blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
XX Alzheimer's disease; atherosclerosis; restenosis; heavy chain; ds.
XX OS Homo sapiens.
XX PN WO2004050850-A2.
XX PD 17-JUN-2004.
XX PF 02-DEC-2003; 2003WO-US038234.
XX PR 02-DEC-2002; 2002US-0430724P.
XX PA (ABGE-) ABGENIX INC.
XX PA (LEXI-) LEXICON GENETICS INC.
XX PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Peng X;
XX Jia X, Nocerini MR;
XX WPI; 2004-461119/43.
XX DR
XX PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
XX useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
XX asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX Example 5; SEQ ID NO 48; 128pp; English.
XX The invention comprises a human monoclonal antibody that binds to
XX phospholipase A2 (PLA2). The monoclonal antibody of the invention is
XX useful in the preparation of a medicament for the treatment of
XX inflammatory and degenerative disorders stemming from inflammatory
XX reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
XX asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
XX nucleic acid represents a human PLA2-specific monoclonal antibody heavy
XX chain DNA sequence.
XX SQ Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 GGATCAACTCTGG 31
DB 1 GGATACAGCTATGG 14

RESULT 200
ADP47135
ID ADP47135 standard; DNA; 15 BP.
XX AC ADP47135;
XX AC
XX DT 09-SEP-2004 (first entry)
XX DE Human phospholipase A2-specific mAb heavy chain DNA sequence #15.

```

XX human; monoclonal antibody; phospholipase A2; PLA2;  
 KW inflammatory disorder; degenerative disorder;  
 XX joint inflammatory reaction; skin inflammatory reaction;  
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;  
 XX Alzheimer's disease; atherosclerosis; restenosis; heavy chain; ds.  
 OS Homo sapiens.  
 XX WO2004050850-A2.  
 XX 17-JUN-2004.  
 XX  
 XX 02-DEC-2003; 2003WO-US038234.  
 XX  
 XX 02-DEC-2002; 2002US-0430724P.  
 XX  
 XX (ABGE-) ABGENIX INC.  
 XX (LEXI-) LEXICON GENETICS INC.  
 XX  
 XX Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;  
 XX Jia X, Nocerini MR;  
 XX WPI; 2004-461119/43.  
 XX  
 XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),  
 XX useful for treating inflammatory conditions, e.g. arthritis, psoriasis,  
 XX asthma, Alzheimer's disease, atherosclerosis, or restenosis.  
 XX  
 XX Example 5; SEQ ID NO 50; 128pp; English.  
 XX  
 XX The invention comprises a human monoclonal antibody that binds to  
 XX phospholipase A2 (PLA2). The monoclonal antibody of the invention is  
 XX useful in the preparation of a medicament for the treatment of  
 XX inflammatory and degenerative disorders stemming from inflammatory  
 XX reactions in the joints, skin, and blood vessels, arthritis, psoriasis,  
 XX asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present  
 XX nucleic acid represents a human PLA2-specific monoclonal antibody heavy  
 XX chain DNA sequence.  
 XX  
 XX Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;  
 XX  
 XX  
 XX Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 XX Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX QY 18 GGATACAACTCTGG 31  
 XX ||||| |||||  
 XX Db 1 GGATACAGCTATGG 14  
 XX  
 XX  
 XX RESULT 201  
 XX ADP47129  
 XX ID ADP47129 standard; DNA; 15 BP.  
 XX AC ADP47129;  
 XX XX  
 XX 09-SEP-2004 (first entry)  
 XX  
 XX Human phospholipase A2-specific mAb heavy chain DNA sequence #9.  
 XX  
 XX human; monoclonal antibody; phospholipase A2; PLA2;  
 KW inflammatory disorder; degenerative disorder;  
 XX joint inflammatory reaction; skin inflammatory reaction;  
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;  
 KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain; ds.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO2004050850-A2.  
 XX 17-JUN-2004.  
 XX

PF 02-DEC-2003; 2003WO-US038234.  
 XX  
 XX 02-DEC-2002; 2002US-0430724P.  
 XX  
 XX (ABGE-) ABGENIX INC.  
 XX (LEXI-) LEXICON GENETICS INC.  
 XX  
 XX Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;  
 XX Jia X, Nocerini MR;  
 XX WPI; 2004-461119/43.  
 XX  
 XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),  
 XX useful for treating inflammatory conditions, e.g. arthritis, psoriasis,  
 XX asthma, Alzheimer's disease, atherosclerosis, or restenosis.  
 XX  
 XX Example 5; SEQ ID NO 44; 128pp; English.  
 XX  
 XX The invention comprises a human monoclonal antibody that binds to  
 XX phospholipase A2 (PLA2). The monoclonal antibody of the invention is  
 XX useful in the preparation of a medicament for the treatment of  
 XX inflammatory and degenerative disorders stemming from inflammatory  
 XX reactions in the joints, skin, and blood vessels, arthritis, psoriasis,  
 XX asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present  
 XX nucleic acid represents a human PLA2-specific monoclonal antibody heavy  
 XX chain DNA sequence.  
 XX  
 XX Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;  
 XX  
 XX  
 XX Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 XX Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX QY 18 GGATACAACTCTGG 31  
 XX ||||| |||||  
 XX Db 1 GGATACAGCTATGG 14  
 XX  
 XX  
 XX RESULT 202  
 XX ADP47122  
 XX ID ADP47122 standard; DNA; 15 BP.  
 XX AC ADP47122;  
 XX XX  
 XX 09-SEP-2004 (first entry)  
 XX  
 XX Human phospholipase A2-specific mAb heavy chain DNA sequence #2.  
 XX  
 XX human; monoclonal antibody; phospholipase A2; PLA2;  
 KW inflammatory disorder; degenerative disorder;  
 KW joint inflammatory reaction; skin inflammatory reaction;  
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;  
 KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain; ds.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO2004050850-A2.  
 XX 17-JUN-2004.  
 XX  
 XX 02-DEC-2003; 2003WO-US038234.  
 XX  
 XX 02-DEC-2002; 2002US-0430724P.  
 XX  
 XX (ABGE-) ABGENIX INC.  
 XX (LEXI-) LEXICON GENETICS INC.  
 XX  
 XX Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;  
 XX Jia X, Nocerini MR;  
 XX WPI; 2004-461119/43.  
 XX  
 XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),

PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,  
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.  
 PS Example 5; SEQ ID NO 37; 128pp; English.  
 XX  
 CC The invention comprises a human monoclonal antibody that binds to  
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is  
 CC useful in the preparation of a medicament for the treatment of  
 CC inflammatory and degenerative disorders stemming from inflammatory  
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,  
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present  
 CC nucleic acid represents a human PLA2-specific monoclonal antibody heavy  
 CC chain DNA sequence.  
 XX  
 SQ Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 95.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 18 GGATACAACTCTGG 31  
 DB 1 GGATACAGCTATGG 14  
 RESULT 203  
 AEB19896/C  
 ID AEB19896 standard; DNA; 15 BP.  
 XX  
 AC AEB19896;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE PCR primer #1.  
 XX  
 KW Microorganism detection; PCR; primer; intestine infection;  
 KW gastrointestinal-gen.; gastrointestinal disease; infection; ss.  
 XX  
 OS Vibrio fluvialis.  
 XX  
 FN CN1560273-A.  
 PD 05-JAN-2005.  
 XX  
 PF 26-FEB-2004; 2004CN-00015461.  
 XX  
 PR 26-FEB-2004; 2004CN-00015461.  
 XX  
 PA (UYZH-) UNIV ZHONGSHAN.  
 XX  
 PI Deng X, He J, Wang Z;  
 XX  
 DR WPI; 2005-296834/31.  
 XX  
 PT Kit for diagnosing gene of pathogenic bacterial and river vibron of  
 PT aquatic animal and human and testing method thereof.  
 XX  
 PS Claim 1; Page 2; 7pp; Chinese.  
 XX  
 CC The invention relates to a kit for detecting aquatic animal pathogens and  
 CC human pathogens, comprising a pair of PCR primers used to detect specific  
 CC DNA fragments of *Vibrio fluvialis*. The kit and method can be used in  
 CC bacteria tracking and detection of aquatic animal pathogens in the course  
 CC of breeding and also in the clinical detection of human intestinal acute  
 CC infections, as well as in environmental monitoring. This sequence  
 XX represents a PCR primer used in the scope of the invention.  
 SQ Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 14.0%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 TCCTCTGAGAGGTA 47  
 DB 15 TCCTCTGGGAGAA 2  
 RESULT 204  
 AAN92945  
 ID AAN92945 standard; DNA; 12 BP.  
 XX  
 AC AAN92945;  
 XX  
 DT 01-JUL-1990 (first entry)  
 XX  
 DE Consensus sequence for mammalian expression vector.  
 XX  
 KW Murine autonomously replicating sequence; consensus sequence;  
 KW mammalian expression vector.  
 XX  
 OS Mouse.  
 XX  
 PN EP306848-A.  
 XX  
 PD 15-MAR-1989.  
 XX  
 PF 02-SEP-1988; 88EP-00114317.  
 XX  
 PR 09-SEP-1987; 87DE-03730246.  
 XX  
 PA (BOEP ) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Grummt F, Weidle U;  
 XX  
 DR WPI; 1989-078357/11.  
 XX  
 PT Expression vectors for mammalian cells - with two consensus sequences and  
 PT inefficient selection system.  
 XX  
 PS Claim 2; Page 8; 12pp; German.  
 XX  
 CC The inventors claim vectors for the expression of heterologous proteins  
 CC in mammalian cells. Each vector has a first and second consensus sequence  
 CC (CS). The CS or their homologues are present in known murine autonomously  
 CC replicating sequences (MuARS). The first CS is homologous to AAN92945.  
 CC The inefficient selection system comprises the tk gene and a truncated tk  
 CC promoter. The vectors also contain a gene coding for a protein and the  
 CC necessary promoter and terminator sequences for the expression of this  
 CC gene. The expression vectors provide rapid amplification, allow selection  
 CC of best clones in a short time, are of universal utility in mammalian  
 CC cells, and are free of viral origin sequences  
 SQ Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 13.5%; Score 10.4; DB 1; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 36 CTCTGAGAGGTA 47  
 DB 1 CTCTGAGAGAA 12  
 RESULT 205  
 ABI24047/C  
 ID ABI24047 standard; DNA; 12 BP.  
 XX  
 AC ABI24047;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 324020 for detecting SNP TSC0031735.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 PN 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 324020; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 12 BP; 0 A; 6 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 13.5%; Score 10.4; DB 1; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 50 GAGCCAGCGAAG 61  
 Db 12 GAGCGAGCGAAG 1  
 |||||  
 RESULT 206  
 ABH85885/c  
 ID ABH85885 standard; DNA; 12 BP.  
 XX AC ABH85885;  
 XX 22-FEB-2002 (first entry)  
 XX Oligonucleotide primer SEQ ID NO 285878 for detecting SNP TSC0012487.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 285878; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;  
 Query Match 13.5%; Score 10.4; DB 1; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 40 GAGAGGTAAAGA 51  
 Db 12 GAGAGGTAAAGA 1  
 |||||  
 RESULT 207  
 ABI17646  
 ID ABI17646 standard; DNA; 12 BP.  
 XX AC ABI17646;  
 XX 22-FEB-2002 (first entry)  
 XX Oligonucleotide primer SEQ ID NO 317619 for detecting SNP TSC0028141.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 317619; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)



CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 41 AGAGGTAAGAG 52  
 Db 1 AAAGGTAAGAG 12  
 |||||

RESULT 208  
 ABI18779  
 ID ABI18779 standard; DNA; 12 BP.  
 AC ABI18779;  
 XX  
 XX 22-FEB-2002 (first entry)  
 DT  
 XX  
 XX Oligonucleotide primer SEQ ID NO 318752 for detecting SNP TSC0028845.  
 DE  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 PN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PT  
 XX Claim 1; SEQ ID NO 318752; 29pp + Sequence Listing; German.  
 PS  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAG 50  
 Db 1 TGAGAGATAAG 12  
 |||||

RESULT 209  
 ABI33596/C  
 ID ABI33596 standard; DNA; 12 BP.  
 XX  
 AC ABI33596;  
 AC  
 XX 22-FEB-2002 (first entry)  
 DT  
 XX  
 XX Oligonucleotide primer SEQ ID NO 333569 for detecting SNP TSC0037605.  
 DE  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 PN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PT  
 XX Claim 1; SEQ ID NO 333569; 29pp + Sequence Listing; German.  
 PS  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAG 50  
 Db 12 TGAGAGATAAG 1  
 |||||

RESULT 210  
 AAX22517  
 ID AAX22517 standard; RNA; 13 BP.  
 XX



```

AC AAX22517;
XX
XX 25-MAR-2003 (revised)
DT 21-MAY-1999 (first entry)
XX
XX Streptomyces sp. aac7 gene RBS RNA fragment.
DE
XX
XX Xylanase; acidophilic; thermostable; XYL I; XYL II; plant biomass;
KW hemicellulase; beta-1,4 bond; xylosic chain; xylan; D-xylose; paper;
KW pulp; chlorine bleaching; feed; beta-glucan; cellulose; lignin; ds.
XX
XX Streptomyces sp.
OS
XX
XX US5871730-A.
FN
XX
XX 16-FEB-1999.
PD
XX
XX 29-JUL-1994; 94US-00282197.
PF
XX
XX 29-JUL-1994; 94US-00282197.
PR
XX
XX (UYSH ) UNIV SHERBROOKE.
PA
XX
XX Beaulieu C, Brzezinski R, Dery CV;
PI
XX
XX WPI; 1996-141348/14.
DR
XX
XX New acidophilic and thermostable xylanase enzymes from Actinomadura sp.
XX FC7 - useful for treating plant biomass, especially paper and wood pulp,
XX PT to degrade hemicellulose and hydrolyse xylan.
XX
XX
XX Example 7; Fig 7; 60pp; English.
XX
XX This invention describes the use of novel acidophilic and thermostable
XX xylanase enzymes (XYL I and XYL II) from Actinomadura sp. FC7 which
XX retain their activity under harsh industrial conditions (e.g. high
XX temperature or wide pH ranges) and may be secreted by recombinant host
XX cells, to treat plant biomass. Xylanases XYL I and XYL II are part of a
XX large group of hemicellulase enzymes and function by cutting the beta-1,4
XX bonds within the xylosic chain of xylan (a polymer of D-xylose residues
XX that is a major constituent of hemicellulose). This means that they may
XX be used in the paper and pulp industry to improve the efficiency of the
XX bleaching process by degrading the structure of the material. XYL I and
XX XYL II may also be used to treat feed, by degrading a substrate with a
XX high beta-glucan or cellulose content. XYL I and XYL II retain their
XX activity at high temperatures (e.g. 70 deg. C) and at low pHs (e.g. 4.0),
XX conditions which tend to denature most known xylanases. Enzymes that
XX remain active in these conditions may be used in industrial processes
XX that are carried out at high temperature and low pH to speed up other,
XX non-enzymatic reactions, minimising costs, energy requirements, and the
XX risk of pollution, (e.g. enzymes XYL I and XYL II can be used to
XX facilitate chlorine bleaching of paper pulp which is carried out in hot,
XX acidic conditions). Pretreatment with XYL I and XYL II, allows the
XX bleaching agents to penetrate better, to remove lignin from the pulp and
XX 'bleach' the colouration from it. This means smaller quantities of the
XX agents can be used to produce the same or a better result. Also,
XX disrupting the structure aids water drainage. NOTE: This patent is an
XX equivalent to FI9503640. (Updated on 25-MAR-2003 to correct DR field.)
XX
XX
XX Sequence 13 BP; 2 A; 4 C; 5 G; 0 T; 2 U; 0 Other;
SQ
Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 56 GCGAAGCTGATG 67
    |||||:|:|
Db 2 GCGACGCGAUG 13

RESULT 211
AAC88504
ID AAC88504 standard; RNA; 13 BP.

AAC88504;
02-MAR-2001 (first entry)
Murine pl6 coding sequence fragment.
Ribozyme; retinal degradation; retinal disease; learning; memory;
anylotropic lateral sclerosis; tumour suppression; ss.
Mus sp.
WO200066780-A2.
09-NOV-2000.
28-APR-2000; 2000WO-US011509.
30-APR-1999; 99US-0131942P.
(UYFL ) UNIV FLORIDA.
Lewin AS, Muzyczka N, Hauswirth WM, Teschendorf C, Burger C;
WPI; 2000-687548/67.
Novel methods for identifying genes with selected functions comprising
contacting genes with a library of ribozymes, useful for identifying
genes involved in, e.g. retinal disease, learning or memory and tumor
suppression.
Claim 16; Fig 7; 111pp; English.
The present invention relates to a method for identifying a gene with a
selected function comprising contacting genes with a library of ribozymes
and identifying at least 1 ribozyme that alters the selected function of
the gene. The present sequence is a target sequence used in the present
invention. The methods (and ribozymes) are useful for identifying novel
genes involved in retinal degradation, retinal disease, learning or
memory, amyotrophic lateral sclerosis or tumour suppression, and for
producing non-human animal models of diseases
Sequence 13 BP; 1 A; 4 C; 5 G; 0 T; 3 U; 0 Other;
SQ
Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 29 TCGAGTCCTCTG 40
    :|||:|:|
Db 1 UCGAGUCGCGUG 12

RESULT 212
ABH39407/c
ID ABH39407 standard; DNA; 13 BP.
AC ABH39407;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 239384 for detecting SNP TSC0058391.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX

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PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 239384; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
SQ
Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTTAAAG 50
Db 12 TGAGAGATAAAG 1
||||| |||||

RESULT 213
ABF32921/c
ID ABF32921 standard; DNA; 13 BP.
XX
AC ABF32921;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 132918 for detecting SNP TSC0033164.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 132918; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 5 C; 0 G; 5 T; 0 U; 0 Other;
SQ
Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTTAAAG 50
Db 12 TGAGAGGTTAAAG 1
||||| |||||

RESULT 214
ABF46225/c
ID ABF46225 standard; DNA; 13 BP.
XX
AC ABF46225;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 146222 for detecting SNP TSC0036842.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 146222; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 5 C; 0 G; 5 T; 0 U; 0 Other;
SQ
Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTTAAAG 50
Db 12 TGAGAGGTTAAAG 1
||||| |||||

RESULT 215
ABF32921/c
ID ABF32921 standard; DNA; 13 BP.
XX
AC ABF32921;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 132918 for detecting SNP TSC0033164.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

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CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match      13.5%; Score 10.4; DB 1; Length 13;
  Best Local Similarity 91.7%; Pred. No. 1.3e+02;
  Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAG 50
Db 13 TGAGAGGTAAG 2

RESULT 215
ABH04743/c
ID ABH04743 standard; DNA; 13 BP.
XX
XX ABH04743;
AC
AC ABH04743;
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 204720 for detecting SNP TSC0050222.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
DT
XX
XX 06-APR-2001; 2001WO-IB000713.
DE
XX
XX 07-APR-2000; 2000DE-01019173.
DT
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 204720; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 1 Other;

  Query Match      13.5%; Score 10.4; DB 1; Length 13;
  Best Local Similarity 91.7%; Pred. No. 1.3e+02;
  Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAG 50
Db 13 TGAGAGGTAAG 2

RESULT 216
ABH39406
ID ABH39406 standard; DNA; 13 BP.
XX
XX ABH39406;
AC
AC ABH39406;
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 239383 for detecting SNP TSC0058391.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
DT
XX
XX 06-APR-2001; 2001WO-IB000713.
DE
XX
XX 07-APR-2000; 2000DE-01019173.
DT
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 239383; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match      13.5%; Score 10.4; DB 1; Length 13;
  Best Local Similarity 91.7%; Pred. No. 1.3e+02;
  Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAG 50
Db 2 TGAGAGGTAAG 13

RESULT 217
ABF32920
ID ABF32920 standard; DNA; 13 BP.
XX
XX ABF32920;
AC
AC ABF32920;
XX
XX 21-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 132917 for detecting SNP TSC0033164.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

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KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 139917; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 13.5%; Score 10.4; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 39 TGAGAGGTTAAG 50  
 Db 2 TGAGAGGTTAAG 13  
 |||||  
 RESULT 218  
 ABP95653/C  
 ID ABP95653 standard; DNA; 13 BP.  
 XX  
 AC ABP95653;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 195650 for detecting SNP TSC0048132.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.  
 XX Claim 1; SEQ ID NO 195650; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 13.5%; Score 10.4; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 41 AGAGGTTAAGAG 52  
 Db 13 AGAGGTTAAGTG 2  
 |||||  
 RESULT 219  
 ABH04742  
 ID ABH04742 standard; DNA; 13 BP.  
 XX  
 AC ABH04742;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 204719 for detecting SNP TSC0050222.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.  
 XX Claim 1; SEQ ID NO 204719; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 13.5%; Score 10.4; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 41 AGAGGTTAAGAG 52  
 Db 13 AGAGGTTAAGTG 2  
 |||||  
 RESULT 219  
 ABH04742  
 ID ABH04742 standard; DNA; 13 BP.  
 XX  
 AC ABH04742;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 204719 for detecting SNP TSC0050222.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.  
 XX Claim 1; SEQ ID NO 204719; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 13.5%; Score 10.4; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 41 AGAGGTTAAGAG 52  
 Db 13 AGAGGTTAAGTG 2  
 |||||  
 RESULT 219  
 ABH04742  
 ID ABH04742 standard; DNA; 13 BP.  
 XX  
 AC ABH04742;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 204719 for detecting SNP TSC0050222.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.  
 XX Claim 1; SEQ ID NO 204719; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 13.5%; Score 10.4; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 41 AGAGGTTAAGAG 52  
 Db 13 AGAGGTTAAGTG 2  
 |||||  
 RESULT 219  
 ABH04742  
 ID ABH04742 standard; DNA; 13 BP.  
 XX  
 AC ABH04742;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 204719 for detecting SNP TSC0050222.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 1 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAAG 50  
 Db 1 TGAGAGGTAGAG 12

RESULT 220  
 ABC36749/c  
 ID ABC36749 standard; DNA; 13 BP.  
 XX AC ABC36749;  
 XX DT 20-FEB-2002 (first entry)  
 XX DE Oligonucleotide SEQ ID NO 36766 for detecting SNP TSC0011511.  
 XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX DR WPI; 2001-657177/75.  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 36766; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 1 A; 4 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 AGAGGTAAAGAG 52  
 Db 12 AAAGGTAAAGAG 1

RESULT 221  
 ABF13387/c  
 ID ABF13387 standard; DNA; 13 BP.  
 XX AC ABF13387;  
 XX DT 21-FEB-2002 (first entry)  
 XX DE Oligonucleotide SEQ ID NO 113384 for detecting SNP TSC0028368.  
 XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX DR WPI; 2001-657177/75.  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 113384; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 0 A; 7 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 AGAGGTAAAGAG 52  
 Db 13 AGAGGGAAAGAG 2

RESULT 222  
 ABC36748  
 ID ABC36748 standard; DNA; 13 BP.  
 XX











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Query Match      13.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 62 CTGATGTCCTGT 73
DB 1 CUGCUGUCCUGU 12

RESULT 229
AAQ47917
ID AAQ47917 standard; DNA; 10 BP.
XX
AC AAQ47917;
XX
XX 25-MAR-2003 (revised)
DT 23-MAR-1994 (first entry)
XX
XX Primer for production of cDNA from mRNA.
DE
XX cDNA; mRNA; primer; PCR; polymerase chain reaction; poly A site; RT;
XX reverse transcriptase; kozak sequence; ss.
XX
XX Synthetic.
OS
XX WO9318176-A1.
XX
XX 16-SEP-1993.
XX
XX 11-MAR-1993; 93WO-US002246.
XX
XX 11-MAR-1992; 92US-00850343.
PR 11-MAR-1993; 93US-00033084.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
PA
XX Liang P, Pardee AB;
PI
XX WPI; 1993-303488/38.
XX
XX Cloning and isolating mRNA as cDNA - by reverse transcription and
PT polymerase amplification using two oligo-deoxy-nucleotide(s).
XX
XX Example 4; Page 17; 43pp; English.
PS
XX Two primers are used to amplify any given mRNA molecule in its cDNA form.
CC The first primer is capable of binding either to (1) a site immediately
CC upstream of the first adenine nucleotide of the poly A tail, (2) to a
CC site including the mRNA's poly A signal sequence; (3) to a site including
CC the mRNA's Kozak sequence or (4) to a sequence of an mRNA of which the
CC nucleotide sequence is known. These primers are then extended by reverse
CC transcriptase to produce the corresponding cDNA sequence. The second
CC primer comprises an arbitrary sequence and is used alongside the first
CC primer to amplify the cDNA molecule by PCR. This primer is a second
CC arbitrary primer. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
DB 1 AGCCAGCGAA 10

RESULT 231
AAT18616
ID AAT18616 standard; DNA; 10 BP.
XX
AC AAT18616;
XX
XX 06-NOV-1996 (first entry)
DT
XX
XX Arbitrary 5' oligodecamer DDRT-PCR primer OPA 16.
XX
XX Differential display of mRNA; reverse transcription; DDRT-PCR; human;
KW chondrocyte; gene specific; primer; probe; isolation; interleukin-1beta;
KW IL-1beta; diagnosis; connective tissue disease; osteoarthritis;
KW rheumatoid arthritis; polymerase chain reaction; ss.
XX
XX Synthetic.
OS
XX EF705842-A2.
XX
XX 10-APR-1996.
PD
XX
XX 02-OCT-1995; 95EP-00115510.
PF
XX

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XX
DT 12-FEB-1996 (first entry)
XX
DB Syngeneic and allogeneic transplant comparison primer, OPA-16.
XX
XX AIP-1; allograft inflammatory factor 1; transplant rejection; inhibitor;
KW immunogenic; detection; diagnosis; ss.
XX
XX Synthetic.
OS
XX WO9517506-A1.
XX
XX 29-JUN-1995.
PD
XX
XX 21-DEC-1994; 94WO-US014724.
PF
XX
XX 21-DEC-1993; 93US-00171385.
PR
XX (HARD ) HARVARD COLLEGE.
XX
XX Russell MB, Utans U;
PI
XX WPI; 1995-240668/31.
XX
XX DNA encoding allograft rejection factors and immunogenic fragments -
PT useful for identifying transplant rejection inhibitors.
XX
XX Disclosure; Page 12; 138pp; English.
XX
XX AAQ99394-Q99396 are primers used to identify DNA from both allogeneic and
CC syngeneic sources to determine where a specific gene is expressed. The
CC AIP-1 gene is a differentially expressed allograft gene which is
CC expressed in allograft tissue during transplant rejection. Identification
CC of the AIP-1 product (AAR80520) or transcript indicates that allograft
CC rejection is taking place. The human AIP-1 gene and product are therefore
CC useful in the diagnosis of transplant rejection. The diagnostic methods
CC used allow rejection (vascular inflammation) to be detected at an early
CC stage and require only a small amount of biopsy material
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
DB 1 AGCCAGCGAA 10

RESULT 231
AAT18616
ID AAT18616 standard; DNA; 10 BP.
XX
AC AAT18616;
XX
XX 06-NOV-1996 (first entry)
DT
XX
XX Arbitrary 5' oligodecamer DDRT-PCR primer OPA 16.
XX
XX Differential display of mRNA; reverse transcription; DDRT-PCR; human;
KW chondrocyte; gene specific; primer; probe; isolation; interleukin-1beta;
KW IL-1beta; diagnosis; connective tissue disease; osteoarthritis;
KW rheumatoid arthritis; polymerase chain reaction; ss.
XX
XX Synthetic.
OS
XX EF705842-A2.
XX
XX 10-APR-1996.
PD
XX
XX 02-OCT-1995; 95EP-00115510.
PF
XX

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PR 06-OCT-1994; 94EP-00115751.
XX (FARH ) HOECHST AG.
XX Bartnik E, Margerie D;
XX WPI; 1996-181045/19.
XX
XX Diagnosis and treatment of IL-1 mediated connective tissue diseases -
PT using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or
PT antibodies to them.
XX
XX Example; Page 15; 31pp; English.
XX
XX The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which
XX were used along with 4 degenerate 3' oligo dt primers for the
XX differential display of human chondrocyte mRNA by reverse transcription
XX and PCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA
XX clones, which were then searched against DNA databases for homology to
XX known human genes. The cDNA mols. can be used for the prodn. of gene
XX specific primers and probes to isolate genes induced by treating (esp.
XX human) chondrocytes with interleukin-1beta (IL-1beta), and for the
XX diagnosis of IL-1beta related connective tissue diseases, in partic.
XX osteoarthritis or rheumatoid arthritis
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
DB 1 AGCCAGCGAA 10
|||||
RESULT 232
AAT75144
ID AAT75144 standard; DNA; 10 BP.
XX
XX AAT75144;
AC
XX
XX 04-MAR-1998 (first entry)
DT Arbitrary RT-PCR primer.
DE
XX
XX dhc-1; homocysteine; hypohomocysteinaemia; atherosclerosis; diagnosis;
XX serum; Dami cell; PCR; arbitrary primer; messenger RNA pool; ss.
XX
XX Synthetic.
OS
XX
XX WO9725440-A2.
PN
XX
XX 17-JUL-1997.
PD
XX
XX 02-JAN-1997; 97WO-CA000001.
PF
XX
XX 03-JAN-1996; 96US-00582261.
PR
XX (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
PA
XX
XX Austin RC, Hirsch J, Weitz J;
PI
XX
XX WPI; 1997-372877/34.
DR
XX
XX Methods and polynucleotide(s) for diagnosing hyperhomocysteinaemia -
PT and/or predisposition to develop premature atherosclerosis by detecting
PT increased levels of serum homocysteine.
XX
XX Disclosure; Page 22; 84pp; English.
PS
XX Arbitrary RT-PCR primers (AAT75138-42) were used to amplify mRNA from
XX cells exposed to hyperphysiological, normal or subphysiological levels of
XX

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CC homocysteine. PCR products were separated on a sequencing gel and
CC discrete fractions which were increased or decreased were identified.
CC This method was used to identify mRNA and the corresponding cDNA which
CC are increased in the cells of a patient having hyperhomocysteinaemia or a
CC predisposition to homocysteine mediated atherosclerosis. These
CC polynucleotides can be used for the diagnosis and treatment of
CC atherosclerotic diseases and diseases of metabolism of sulphur containing
CC amino acids (e.g. homocysteinaemia), which are associated with vascular
CC damage and atherosclerotic disease, specifically unstable angina, acute
CC myocardial infarction (heart attack), cerebrovascular accidents (stroke),
CC hypertension, renal artery stenosis, aortic stenosis and deep vein
CC occlusive disease
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
DB 1 AGCCAGCGAA 10
|||||
RESULT 233
AAV10688
ID AAV10688 standard; DNA; 10 BP.
XX
XX AAV10688;
AC
XX
XX 21-JUL-1998 (first entry)
DT
XX
XX Human breast cancer gene differential display primer #6.
DE
XX
XX Breast cancer; malignant transformation; diagnostic; therapeutic;
XX screening; primer; ss.
XX
XX Synthetic.
OS
XX
XX Homo sapiens.
OS
XX
XX WO9738085-A2.
PN
XX
XX 16-OCT-1997.
PD
XX
XX 09-APR-1997; 97WO-US005930.
PF
XX
XX 10-APR-1996; 96US-0015167P.
PR
XX 05-JUN-1996; 96WO-US009286.
PR
XX 06-JUN-1996; 96US-0019202P.
PR
XX 11-JUL-1996; 96US-00678280.
PR
XX (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
PA
XX
XX Smith H, Chen L;
PI
XX
XX WPI; 1997-512705/47.
DR
XX
XX Breast cancer genes - used to develop products to design or screen
PT diagnostic reagents or therapeutic compounds.
PT
XX
XX Example 2; Page 46; 118pp; English.
PS
XX
XX Primers AAV10683-V10688 are used to obtain novel human breast cancer
XX genes by differential display. The identified genes or fragments of these
XX genes can be used for identifying genes and gene products that are
XX intimately related to malignant transformation or maintenance of the
XX malignant properties of cancer cells. It can also be used to design or
XX screen diagnostic reagents or therapeutic compounds. Kits are included
XX within the scope of the invention
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 234
AAV15590
ID AAV15590 standard; DNA; 10 BP.
AC AAV15590;
XX
DT 02-JUL-1998 (first entry)
DE Human HPK-1A C4.8 and C21.7 PCR primer AP-1.
KW Cervical cancer; treatment; diagnosis; passage cell; lesion;
KW human foreskin keratinocyte cell line; HPK-1A; antibody; smear;
KW PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN DE19649207-C1.
XX
PD 26-FEB-1998.
XX
PF 27-NOV-1996; 96DE-01049207.
XX
PR 27-NOV-1996; 96DE-01049207.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Duerst M, Nees M;
XX
XX WPI; 1998-121623/12.
XX
XX Nucleic acid characteristic of late or early passage cells immortalised
PT by papilloma virus - and related polypeptide(s) and antibodies, used for
PT diagnosis and treatment of cervical cancer and assessing potential for
PT progression of cervical lesions.
XX
XX Example 1; Page 4; 8pp; German.
XX
XX PCR primers AAV15590 and AAV15591 are used to amplify fragments of the
CC C4.8 and C21.7 genes from a human papillomavirus (HPV) immortalised human
CC foreskin keratinocyte cell line HPK-1A. These genes are characteristic of
CC late or early passage cells and can be used in a method for assessing the
CC potential for progression of cervical lesions. Antibodies generated
CC against the encoded polypeptide are used for diagnosis of cervical cancer
CC and to assess potential for lesion progression. Antibodies can also be
CC used therapeutically by inhibiting the polypeptide. Antisense molecules
CC based on the nucleotide sequence are used to inhibit expression of the
CC protein. Detecting polypeptides, or related RNA, characteristic of late
CC passage cells (which are potentially malignant) in cervical smears is a
CC reliable way of assessing progression potential
XX
SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 235
AAV15590
ID AAV15590 standard; DNA; 10 BP.
AC AAV15590;
XX
DT 10-JAN-2000 (first entry)
DE Arbitrary primer A.
XX
XX Signal transduction protein; dehiscence; male sterile plant;
KW shatter resistance; oilseed rape; primer; ss.
XX
OS Synthetic.
XX
FN WO9949046-A1.
XX
PD 30-SEP-1999.
XX
PF 22-MAR-1999; 99WO-GB000905.
XX
PR 20-MAR-1998; 98GB-00006113.
XX

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XX AAX34945;
XX
DT 28-JUN-1999 (first entry)
DE PCR primer for DNA encoding a dehiscence zone protein ORS7(9).
KW Dehiscence zone protein; ORS7(9); regulation; pod dehiscence;
KW plant abscission; PCR primer; ss.
XX
OS Synthetic.
OS Brassica napus.
XX
FN WO9915680-A1.
XX
PD 01-APR-1999.
XX
PF 18-SEP-1998; 98WO-GB002836.
XX
PR 19-SEP-1997; 97GB-00020038.
XX
PA (BIOG-) BIOGEMMA UK LTD.
XX
PI Paul W, Roberts JA, Whitelaw C;
XX
XX WPI; 1999-244427/20.
XX
XX New Brassica napus nucleic acid and protein, useful for regulating pod
PT dehiscence and/or plant abscission by producing transgenic plants or
PT propagating material.
XX
XX Example 1; Page 10; 20pp; English.
XX
XX PCR primer AAX34944-45 were used to amplify DNA encoding a dehiscence
CC zone protein designated ORS7(9). The ORS7(9) polynucleotides and
CC polypeptides are useful for regulating pod dehiscence and plant
CC abscission. Antisense ORS7(9) nucleic acid useful for preventing or
CC reducing dehiscence or abscission
XX
SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 236
AAZ22961
ID AAZ22961 standard; DNA; 10 BP.
XX
AC AAZ22961;
XX
XX 10-JAN-2000 (first entry)
DT
XX Arbitrary primer A.
XX
XX Signal transduction protein; dehiscence; male sterile plant;
KW shatter resistance; oilseed rape; primer; ss.
XX
OS Synthetic.
XX
FN WO9949046-A1.
XX
PD 30-SEP-1999.
XX
PF 22-MAR-1999; 99WO-GB000905.
XX
PR 20-MAR-1998; 98GB-00006113.
XX

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PA (BIOG-) BIOEMMA UK LTD.  
 XX Wyatt P, Roberts JA, Whitelaw C;  
 XX WPI; 1999-580449/49.  
 DR A nucleic acid encoding a signal transduction protein involved in plant  
 PT dehiscence, useful for producing shatter resistant male sterile plants.  
 XX Example 1; Page 23; 71pp; English.  
 XX The invention provides a nucleic acid encoding a signal transduction  
 CC protein involved in the process of dehiscence. The nucleic acids and  
 CC proteins are useful for regulating or controlling dehiscence of a pod or  
 CC an anther in a plant, useful in the production of male sterile plants.  
 CC The methods, etc. may be used in production of shatter resistance or  
 CC shatter-delayed plants such as oilseed rape (Brassica napus)  
 XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 13.0%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 51 AGCCAGCGAA 60  
 DB 1 AGCCAGCGAA 10  
 |||||  
 RESULT 237  
 AAX26829  
 ID AAX26829 standard; DNA; 10 BP.  
 XX AAX26829;  
 AC  
 XX 22-JUN-1999 (first entry)  
 DT PCR primer AP-1 used to amplify Rin2 cDNA sequences.  
 DE Rin2; downregulation; functional response; allergy; asthma; hayfever;  
 XX Ras-dependent signalling pathway; allergy; asthma; hayfever;  
 KW atopic eczema; Ras-dependent cancer; neoplastic cellular proliferation;  
 KW autoimmune disease; T cell-associated disease;  
 KW T cell dependent graft vs. host disease; type 1 diabetes mellitus;  
 KW multiple sclerosis; Crohn's disease; autoimmune hepatitis; psoriasis;  
 KW wound healing; angiogenesis; re-epithelialization;  
 KW human immune deficiency virus; immune suppression; cancer therapy;  
 KW nerve regeneration; PCR primer; ss.  
 XX Synthetic.  
 OS  
 XX WO9913079-A1.  
 PN 18-MAR-1999.  
 XX 11-SEP-1998; 98WO-US019056.  
 PF 11-SEP-1997; 97US-0058520P.  
 PR 02-OCT-1997; 97US-00942819.  
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
 PA Tam S, Tsai M, Galli SJ;  
 PI WPI; 1999-229239/19.  
 XX Rin2 polypeptides and related nucleic acid.  
 XX Disclosure; Page 47; 101pp; English.  
 PS The present sequence represents a primer used to amplify Rin2 cDNA  
 CC sequences. Rin2 polypeptides downregulate functional responses elicited  
 CC by Ras-dependent signalling pathways. Agents that increase Rin2 activity

CC (particularly Rin2 itself, optionally expressed from a vector) are used  
 CC to treat allergy (asthma, hayfever or atopic eczema); Ras-dependent  
 CC cancers and (non-)neoplastic cellular proliferation; autoimmune diseases;  
 CC T cell-associated diseases and T cell dependent graft vs. host disease  
 CC (typical examples being type 1 diabetes mellitus; multiple sclerosis;  
 CC Crohn's disease, autoimmune hepatitis and psoriasis). Agents that inhibit  
 CC Rin2 activity are used to improve wound healing; angiogenesis and/or re-  
 CC epithelialization (also to improve immune response to pathogens; in human  
 CC immune deficiency virus, and some other, infections; immune suppression  
 CC associated with cancer therapy, and nerve regeneration)  
 XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 13.0%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 51 AGCCAGCGAA 60  
 DB 1 AGCCAGCGAA 10  
 |||||  
 RESULT 238  
 AAZ25357  
 ID AAZ25357 standard; DNA; 10 BP.  
 XX AAZ25357;  
 AC  
 XX 17-DEC-1999 (first entry)  
 DT Rat DRM PCR primer #1.  
 DE DRM; secreted protein; cell growth inhibition; fusion protein; tumour;  
 XX green fluorescent protein; GFP; hyperproliferative cell disorder;  
 KW enhanced green fluorescent protein; EGFP; diagnosis; PCR primer; ss.  
 XX Synthetic.  
 OS Rattus sp.  
 XX WO9949041-A1.  
 PN 30-SEP-1999.  
 PD 26-MAR-1999; 99WO-US006675.  
 PF 26-MAR-1998; 98US-0079440P.  
 PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA Blair DG, Clausen PA, Topol LZ, Marx M, Calothy G;  
 PI WPI; 1999-591095/50.  
 DR New isolated nucleic acid encoding DRM protein, for regulation of cell  
 XX growth, particularly treating cancer and.  
 PT Example 1; Page 31; 115pp; English.  
 PS The present invention describes nucleic acids comprising human, murine or  
 CC rat cDNAs encoding DRM proteins (derived from the down-regulated in v-mos  
 CC -transformed cells, drm gene). The nucleic acids, and DRM proteins, are  
 CC useful for arresting cell growth; inhibiting tumour cell growth; treating  
 CC hyperproliferative cellular disorders, either in vivo or ex vivo and  
 CC producing fusion proteins with enhanced green fluorescent protein (EGFP)  
 CC of increased stability (useful in screening assays, protein-protein  
 CC interaction studies, cell labeling and as markers during purification).  
 CC Detecting abnormally low levels of DRM, or the nucleic acids, may be used  
 CC to identify subjects with an increased risk of developing a  
 CC hyperproliferative disease. Fragments of the nucleic acids are useful as  
 CC probes and primers to detect or quantify drm and to screen genomic and  
 CC cDNA libraries. Antibodies raised against DRM can be used to  
 CC detect/quantify DRM in immunoassays. Fusion proteins of DRM and GFP are  
 CC localised to the nucleus (in contrast cytoplasmic localisation of GFP



PT Isolated polynucleotides differentially expressed in antigen-presenting  
 XX cells, useful in gene vaccines against cancer.  
 PS Claim 1; Page 125; 130pp; English.  
 XX  
 CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
 CC expression) tags used to identify mRNA transcripts encoding  
 CC immunostimulatory cofactor proteins which are preferentially or  
 CC differentially expressed in monocyte-derived dendritic cells compared  
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
 CC (expressed sequence tags) which were previously unknown to be  
 CC preferentially or differentially expressed in dendritic cells, while  
 CC other transcripts correspond to novel genes. Antigen-presenting cell  
 CC (APC)-associated costimulatory factors play an important role in the  
 CC activation of the cytotoxic immune response, particularly against tumour  
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
 CC complex) and subsequent recognition by T-cell receptors is alone  
 CC insufficient to activate a robust cytotoxic immune response that can lyse  
 CC the tumour cells, immunostimulatory cofactors also being required for  
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
 CC sequences identified using the SAGE tags have several potential uses.  
 CC They may be used in vaccines to induce an immune response, particularly  
 CC against a tumour antigen; to modulate the genotype of an APC; to screen  
 CC for agents that modulate expression of differentially expressed genes in  
 CC an APC; and as hybridisation probes/amplification primers for the  
 CC diagnosis, prognosis and monitoring of diseases related to abnormal  
 CC expression of these genes. Detection of the dendritic cell differentially  
 CC expressed genes, or of their encoded proteins, can be used to identify  
 CC cells as belonging to the monocyte lineage. Cells containing these genes  
 CC can be used in active immunotherapy (or to stimulate production of a  
 CC population of antigen-specific effector cells) and vectors containing  
 CC them are used in gene therapy. Co-administration of tumour antigens and  
 CC APC-associated costimulatory factors ensures adequate antigen  
 CC presentation to endogenous APCs and upregulates the APCs for the  
 CC secretion of co-stimulatory signals, migration to T cell-rich sites,  
 CC recruitment of T cell growth factors and secretion of chemokines for  
 XX recruitment of immune effector cells  
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;  
 Query Match 13.0%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 ACAAGACGGC 13  
 Db 1 ACAAGACGGC 10  
 RESULT 241  
 AAZ50856  
 ID AAZ50856 standard; DNA; 10 BP.  
 XX  
 AC AAZ50856;  
 XX  
 DT 31-MAY-2000 (first entry)  
 XX  
 DE Primer AP1 to identify tobacco salicylic acid inducible genes.  
 XX  
 KW Tobacco plant; salicylic acid inducible gene; fungal pathogen;  
 KW SA-inducible gene; transgenic plant; pathogen resistance; PCR primer; ss.  
 XX  
 OS Nicotiana tabacum.  
 XX  
 FN WO200008186-A1.  
 XX  
 PD 17-FEB-2000.  
 XX  
 PF 02-AUG-1999; 99WO-EP005581.  
 XX  
 PR 03-AUG-1998; 98US-0095187P.  
 XX  
 PA (MOGE-) MOGEN INT NV.

XX Stuiver MH, Jepson I, Horvath DM, Chua N;  
 XX WPI; 2000-205725/18.  
 XX  
 PT Novel salicylic acid inducible genes from tobacco plants, useful for  
 PT making transgenic plants with enhanced pathogenic resistance.  
 XX  
 PS Example 1; Page 51; 57pp; English.  
 XX  
 CC The patent discloses fifteen new salicylic acid (SA) inducible genes from  
 CC Nicotiana tabacum, nine of which were subcloned and sequenced. Based on  
 CC different kinetics of induction response, these genes were classified  
 CC into four categories, class I, II, III and IV response genes. The SA-  
 CC inducible genes are useful for making transgenic plants with enhanced  
 CC pathogen resistance. The plants incorporating these genes show reduced  
 CC susceptibility to fungal pathogens. The present sequence is an upstream  
 CC primer AP1 used in differential display PCR reactions along with  
 CC downstream primers T12MG or T12MC to identify tobacco SA-inducible genes  
 XX  
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;  
 Query Match 13.0%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 51 AGCCAGCGAA 60  
 Db 1 AGCCAGCGAA 10  
 RESULT 242  
 AAZ48447  
 ID AAZ48447 standard; DNA; 10 BP.  
 XX  
 AC AAZ48447;  
 XX  
 DT 27-MAR-2000 (first entry)  
 XX  
 DE Primer specific for C. jejuni.  
 XX  
 KW Microorganism; virus; polymerase chain reaction; food; cosmetic;  
 KW clinical diagnostic; molecular beacon; PCR primer; ss.  
 XX  
 OS Campylobacter jejuni.  
 XX  
 FN WO9963112-A2.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 18-MAY-1999; 99WO-US010940.  
 XX  
 PR 18-MAY-1998; 98US-0086025P.  
 PR 17-MAY-1999; 99US-00086025.  
 XX  
 PA (HUNT-) HUNT WESSON INC.  
 XX  
 PI Romick TL, Fraser MS;  
 XX  
 DR WPI; 2000-086985/07.  
 XX  
 PT Detection of microorganisms and viruses, for use in the food and cosmetic  
 PT industries and for clinical diagnostics.  
 XX  
 PS Disclosure; Page 25; 63pp; English.  
 XX  
 CC The invention provides a novel in vitro method for the detection of  
 CC microorganisms and viruses. The method comprises: (1) forming a  
 CC polymerase chain reaction (PCR) mixture by combining a predetermined  
 CC volume of a sample to be tested for the presence of a nucleic acid  
 CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer  
 CC comprising 5'-GCTAAGGTCCAAAGT-3', and a second primer comprising 5'-  
 CC AGAAGCGCTCTCTACC-3', and PCR reagents; (2) forming a PCR product by

CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,  
 CC to replicate and attain 0.25-10000mg nucleotide product/mul mixture; (3)  
 CC adding a probe containing DNA comprising 5'-GGTGGCTGCTTAAAGCCACC-3' to  
 CC the PCR mixture or to the PCR product to cause the DNA to hybridize with  
 CC the nucleic acid sequence, if present, and change the conformation of the  
 CC probe; and (4) determining whether or not bacteria are present in the  
 CC sample by detecting the conformational change of the probe; a  
 CC conformational change indicating the presence of bacteria in the sample.  
 CC The methods can be used for the detection of viruses and microorganisms,  
 CC including bacteria, yeast, molds and protista. They can be used in the  
 CC food and cosmetic industry and in clinical diagnostics. Using the method  
 CC it is not necessary to remove non-hybridized probe from the system  
 XX  
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60  
 |||||  
 Db 1 AGCCAGCGAA 10

RESULT 243  
 AAA65614  
 ID AAA65614 standard; DNA; 10 BP.

AC AAA65614;

XX 14-NOV-2000 (first entry)

XX Allograft inflammatory factor related PCR primer SEQ ID NO:28.

XX Allograft inflammatory factor 1; AIF-1; AIF-2; allograft gene; screening;  
 KW diagnosis; allograft rejection; vascular inflammation; atherosclerosis;  
 KW immunosuppressive; antiinflammatory; antiarteriosclerotic; PCR primer;  
 XX ss.

OS Rattus sp.

PN US6077948-A.

XX 20-JUN-2000.

XX 21-DEC-1994; 94US-00361441.

XX 21-DEC-1993; 93US-00171385.

XX (HARD ) HARVARD COLLEGE.

XX Utans U, Russell ME;

XX WPI; 2000-430614/37.

XX DNA encoding an allograft inflammatory factor-1, useful for diagnosing  
 PT and treating allograft rejection and other conditions associated with  
 PT vascular inflammation, especially atherosclerosis.

XX Example 1; Col 6; 59pp; English.

XX The present invention describes isolated DNA (I) encoding an allograft  
 CC inflammatory factor-1 (AIF-1). AIF-1 has immunosuppressive,  
 CC antiinflammatory and antiarteriosclerotic activities. AIF-1 is an  
 CC inhibitor of expression of allograft factor such as Gal/GalNAc macrophage  
 CC lectin. AIF-1 is useful for diagnosing and treating allograft rejection  
 CC and other conditions associated to vascular inflammation, especially  
 CC atherosclerosis. The present sequence represents a PCR primer which is  
 CC used in an example from the present invention

XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60  
 |||||  
 Db 1 AGCCAGCGAA 10

RESULT 244  
 AAH63382/c  
 ID AAH63382 standard; cDNA; 10 BP.

XX AAH63382;

XX 20-SEP-2001 (first entry)

XX Human kidney specific transcriptome sequence SEQ ID NO: 222.

XX Human; transcriptome; gene expression pattern; cancer; drug screening;  
 KW cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US031922.

XX 24-NOV-1999; 99US-00448480.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.

XX New isolated polynucleotides, useful for identifying specific cell type,  
 PT such as cancer cell, comprises transcriptomes expressed in particular  
 PT cell types.

XX Claim 11; Page 44; 94pp; English.

XX The present invention describes a method of identifying the type of cell  
 CC in a sample, involving determining which of the sequences AAH63161-  
 CC AAH64724 is expressed by the cell. The transcriptomes described in the  
 CC invention are cell-type specific, cancer specific or ubiquitously  
 CC expressed in humans. They can also be used to screen for drugs, reduce  
 CC cancer specific gene expression, standardise expression and restore the  
 CC function of a diseased cell or tissue. The present sequence is one of the  
 CC transcriptomes described in the exemplification of the invention

XX Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGGCTGGGG 19  
 |||||  
 Db 10 CGGCTGGGG 1

RESULT 245

AAF37532/c

ID AAF37532 standard; DNA; 10 BP.

XX AAF37532;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4271.

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX Saccharomyces cerevisiae.  
 XX WO200077214-A2.  
 XX 21-DEC-2000.  
 XX 14-JUN-2000; 2000WO-US016223.  
 XX 16-JUN-1999; 99US-00335032.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 152; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 13.0%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 47 AAAGAGCCAG 56  
 Db |||||||||  
 10 AAAGAGCCAG 1  
 RESULT 246  
 ID AAF37199/c  
 XX AAF37199 standard; DNA; 10 BP.  
 XX AAF37199;  
 XX 23-MAR-2001 (first entry)  
 DT

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3938.  
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 XX nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX Saccharomyces cerevisiae.  
 XX WO200077214-A2.  
 XX 21-DEC-2000.  
 XX 14-JUN-2000; 2000WO-US016223.  
 XX 16-JUN-1999; 99US-00335032.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 140; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 13.0%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 18 GGATACAACT 27  
 Db |||||||||  
 10 GGATACAACT 1  
 RESULT 247  
 ID AAF36709/c  
 XX AAF36709 standard; DNA; 10 BP.  
 XX





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RESULT 249
AAH77187
ID AAH77187 standard; DNA; 10 BP.
XX
AC AAH77187;
XX
XX 24-JAN-2002 (first entry)
XX
XX Rat arbitrary PCR primer AP-1.
XX
XX Rat; oestrogen agonist-inducible; hUO-44; cytostatic; ovary;
XX uterine cancer; ovarian cancer; uterine growth; uterine; development;
XX ovarian growth; ovarian development; oestrogenic activity; PCR primer;
XX AP-1; ss.
XX
XX Rattus norvegicus.
XX
XX WO200175099-A1.
XX
XX 11-OCT-2001.
XX
XX 04-APR-2001; 2001WO-AU000379.
XX
XX 04-APR-2000; 2000US-0194566P.
XX
XX 15-AUG-2000; 2000AU-00009471.
XX
XX (NACA-) NAT CANCER CENT SINGAPORE PTE LTD.
XX (HUGH/) HUGHES E J L.
XX
XX Huynh TH;
XX
XX WPI; 2002-010789/01.
XX
XX Novel isolated UO-44 nucleic acid molecule useful for treating or
XX diagnosing uterine and/or ovarian cancers, comprises sequence
XX corresponding to uterine estrogen agonist-inducible genetic sequence in
XX mammal.
XX
XX Example 2; Page 37; 82pp; English.
XX
XX The sequence represents the rat arbitrary PCR primer AP-1, used in the
XX invention to amplify cDNA from rat ovary tissue. The invention relates
XX to a novel isolated UO-44 nucleic acid molecule comprising a sequence of
XX nucleotides corresponding to a uterine oestrogen agonist-inducible
XX genetic sequence in a mammal. The UO-44 sequences of the invention have
XX cytostatic activity. The UO-44 polynucleotide is useful in the
XX manufacture of a medicament for the treatment of a condition in a mammal,
XX for treating, diagnosing, detecting or monitoring uterine cancers and/or
XX ovarian cancers, and for producing the polypeptide. The polynucleotide or
XX polypeptide is useful for monitoring uterine and ovarian growth and
XX development and the level of oestrogenic activity in tissue including
XX cancer tissue. They are also useful for the generation of a range of
XX therapeutic molecules capable of modulating oestrogen agonist-mediated
XX cell growth and proliferation in the uterus including ovaries. The UO-44
XX polypeptide is useful to screen for naturally occurring antibodies to
XX itself
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 13.0%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 51 AGCCAGCGAA 60
XX Db 1 AGCCAGCGAA 10
XX
XX RESULT 250
AAH42350
ID AAL42350 standard; DNA; 10 BP.
XX
XX AAL42350;
XX
XX 28-JUN-2002 (first entry)
XX
XX Novel sand pear microsatellite DNA PCR primer 14.
XX
XX Sand pear; ss; PCR; primer; novel microsatellite DNA sequence;
XX Pyrus plant discrimination.
XX
XX Pyrus pyrifolia.
XX
XX JP2002034597-A.
XX
XX 05-FEB-2002.
XX
XX 21-JUL-2000; 2000JP-00220339.
XX
XX 21-JUL-2000; 2000JP-00220339.
XX
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX WPI; 2002-298819/34.
XX
XX A new microsatellite DNA derived from a Pyrus plant and discrimination of
XX Pyrus plants by using it.
XX
XX Example 1; Page 5; 22pp; Japanese.
XX
XX The invention comprises a novel microsatellite DNA sequence derived from
XX Pyrus plants. The invention also comprises a method for discriminating
XX Pyrus plants - utilising the novel Pyrus microsatellite DNA. The novel
XX microsatellite DNA sequence can be used in discriminating Pyrus plants.
XX The present DNA sequence represents a PCR primer specific for a novel
XX Pyrus pyrifolia (sand pear) microsatellite DNA sequence
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 13.0%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 51 AGCCAGCGAA 60
XX Db 1 AGCCAGCGAA 10
XX
XX RESULT 251
ACF12803
ID ACF12803 standard; DNA; 10 BP.
XX
XX ACF12803;
XX
XX 09-SEP-2003 (first entry)
XX
XX Primer used during DBPCR analysis #20.
XX
XX Endometrium; placenta; serine protease; gynecological; cytostatic;
XX cardiant; PRSP; infertility; endometriosis; cancer; pregnancy; primer;
XX PCR; ss.
XX
XX Synthetic.
XX
XX WO2003011905-A1.
XX
XX 13-FEB-2003.
XX
XX 30-JUL-2002; 2002WO-AU001010.
XX
XX 30-JUL-2001; 2001AU-00006707.
XX
XX (PRIN-) PRINCE HENRY'S INST MEDICAL RES.
XX

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PI Nie G, Salamonson LA, Li Y, Hampton AL, Findlay JK;
XX WPI; 2003-268108/26.
XX
XX New nucleic acid encoding a protein having serine protease activity and
XX an insulin-like growth factor-binding motif, useful for preparing a
XX composition for treating a pregnancy-related serum protease-related
XX condition e.g., infertility.
XX
XX Example 1; Page 55; 156pp; English.
XX
XX The present sequence relates to a new isolated nucleic acid molecule,
XX which is expressed in endometrium and placenta and is upregulated in
XX pregnant uterus and is highly expressed during placental development,
XX encodes a protein having serine protease activity and has an insulin-like
XX growth factor (IGF)-binding motif. The compound is considered
XX gynecological, cytostatic and cardiact. The enzyme is specifically
XX expressed in association with embryo implantation and placentaion in a
XX pregnant uterus. The nucleic acid is useful for preparing a composition
XX for treating PRSP-related condition e.g., infertility, endometriosis,
XX cancer or a disease of the heart, testis or ovaries. Further, it is
XX useful for detecting, diagnosing or monitoring a condition involving a
XX change in PRSP expression. The sequence is present in the exemplification
XX of the specification
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
SQ
    Query Match      13.0%; Score 10; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      51 AGCCAGCGAA 60
Db      1 AGCCAGCGAA 10
      |||||
      |||||

RESULT 252
ACF57644/c
ID ACF57644 standard; DNA; 10 BP.
XX
XX ACF57644;
XX
XX 22-APR-2004 (first entry)
XX
XX Human ALDOB gene allele-specific primer SEQ ID NO: 95.
XX
XX Human; ALDOB; fructose-bisphosphate aldolase B; SNP;
XX single nucleotide polymorphism; primer; probe; ss.
XX
XX Homo sapiens.
XX
XX WO2003091454-A1.
XX
XX 06-NOV-2003.
XX
XX 26-APR-2002; 2002WO-US013328.
XX
XX 26-APR-2002; 2002WO-US013328.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Chew A, Kazemi A, Koshiy B;
XX
XX WPI; 2003-877338/81.
XX
XX Claim 41; Page 15; 0pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX fructose-bisphosphate aldolase B (ALDOB) and single nucleotide
XX polymorphisms (SNPs) which have been identified in each sequence. The
XX method of haplotyping the sequences is useful for haplotyping the
XX fructose-bisphosphate aldolase B (ALDOB) gene of an individual or for
XX validating the ALDOB protein as a candidate target for treating a medical

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CC condition predicted to be associated with ALDOB activity. The present
CC sequence is an allele-specific primer/probe used to identify the
CC haplotype of the human ALDOB gene in the exemplification of the invention
XX
XX SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
    Query Match      13.0%; Score 10; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      36 CTCGAGAGG 45
Db      10 CTCGAGAGG 1
      |||||
      |||||

RESULT 253
ADU19679/c
ID ADU19679 standard; DNA; 10 BP.
XX
XX ADU19679;
XX
XX 13-JAN-2005 (first entry)
XX
XX Hypoxia-related tumorigenesis-related SAGE tag #1470.
XX
XX screening; hypoxia-related tumorigenesis;
XX hypoxia-induced gene regulation; tumour; SAGE tag; da.
XX
XX Unidentified.
XX
XX WO2004092198-A2.
XX
XX 28-OCT-2004.
XX
XX 09-APR-2004; 2004WO-US011087.
XX
XX 09-APR-2003; 2003US-0461712P.
XX
XX (GENZ ) GENZYME CORP.
XX
XX Nacht M;
XX
XX WPI; 2004-758333/74.
XX
XX Identifying agents that alter biological activity of a polypeptide
XX encoded by a polynucleotide involved in hypoxia-related tumorigenesis
XX comprises contacting an agent with a target cell and monitoring activity
XX of expressed product.
XX
XX Disclosure; Page 84; 100pp; English.
XX
XX The invention comprises a method of screening for candidate agents
XX capable of altering the biological activity of a protein encoded by a
XX nucleotide involved in hypoxia-related tumorigenesis. The method of the
XX invention involves: contacting a test agent with a target cell expressing
XX the nucleotide, and monitoring the activity of the expressed protein
XX product; if the test agent modifies the activity of the expressed protein
XX then this is a candidate agent. The method of the invention is useful for
XX modifying hypoxia-induced gene regulation and for diagnosing, prognosing
XX or treating tumours. The present DNA sequence represents a SAGE tag that
XX was used in the exemplification of the invention.
XX
XX SQ Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
    Query Match      13.0%; Score 10; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 TACAACCTCTG 30
Db      10 TACAACCTCTG 1
      |||||
      |||||

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RESULT 254
ADU18446/c
ID ADU18446 standard; DNA; 10 BP.
XX AC
XX ADU18446;
XX AC
XX 13-JAN-2005 (first entry)
XX DT
XX Hypoxia-related tumourigenesis-related SAGE tag #237.
XX DE
XX screening; hypoxia-related tumourigenesis;
XX KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX KW
XX Unidentified.
XX OS
XX WO2004092198-A2.
XX PN
XX 28-OCT-2004.
XX PD
XX 09-APR-2004; 2004WO-US011087.
XX PF
XX 09-APR-2003; 2003US-0461712P.
XX PR
XX (GENZ ) GENZYME CORP.
XX PA
XX Nacht M;
XX PI
XX WPI; 2004-758333/74.
XX DR
XX Identifying agents that alter biological activity of a polypeptide
XX encoded by a polynucleotide involved in hypoxia-related tumorigenesis
XX PT comprises contacting an agent with a target cell and monitoring activity
XX of expressed product.
XX PT
XX 28-OCT-2004.
XX PD
XX 09-APR-2004; 2004WO-US011087.
XX PF
XX 09-APR-2003; 2003US-0461712P.
XX PR
XX (GENZ ) GENZYME CORP.
XX PA
XX Nacht M;
XX PI
XX WPI; 2004-758333/74.
XX DR
XX Identifying agents that alter biological activity of a polypeptide
XX encoded by a polynucleotide involved in hypoxia-related tumorigenesis
XX PT comprises contacting an agent with a target cell and monitoring activity
XX of expressed product.
XX PT
XX Disclosure; Page 61; 100pp; English.
XX PS
XX The invention comprises a method of screening for candidate agents
XX capable of altering the biological activity of a protein encoded by a
XX nucleotide involved in hypoxia-related tumorigenesis. The method of the
XX invention involves: contacting a test agent with a target cell expressing
XX the nucleotide, and monitoring the activity of the expressed protein
XX product; if the test agent modifies the activity of the expressed protein
XX then this is a candidate agent. The method of the invention is useful for
XX modifying hypoxia-induced gene regulation and for diagnosing, prognosing
XX or treating tumours. The present DNA sequence represents a SAGE tag that
XX was used in the exemplification of the invention.
XX CC
XX Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
XX SQ
Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 21 TACAACCTCTG 30
XX Db 10 TACAACCTCTG 1
XX
RESULT 255
ADU18244/c
ID ADU18244 standard; DNA; 10 BP.
XX AC
XX ADU18244;
XX AC
XX 13-JAN-2005 (first entry)
XX DT
XX Hypoxia-related tumourigenesis-related SAGE tag #34.
XX DE
XX screening; hypoxia-related tumourigenesis;
XX KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX KW
XX Unidentified.
XX OS
XX WO2004092198-A2.
XX PN
XX 28-OCT-2004.
XX PD
XX 09-APR-2004; 2004WO-US011087.
XX PF
XX 09-APR-2003; 2003US-0461712P.
XX PR
XX (GENZ ) GENZYME CORP.
XX PA
XX Nacht M;
XX PI
XX WPI; 2004-758333/74.
XX DR
XX Identifying agents that alter biological activity of a polypeptide
XX PT
```

PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
 PT comprises contacting an agent with a target cell and monitoring activity  
 of expressed product.

XX Disclosure; Page 56; 100pp; English.

CC The invention comprises a method of screening for candidate agents  
 CC capable of altering the biological activity of a protein encoded by a  
 CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
 CC invention involves contacting a test agent with a target cell expressing  
 CC the nucleotide, and monitoring the activity of the expressed protein  
 CC product; if the test agent modifies the activity of the expressed protein  
 CC then this is a candidate agent. The method of the invention is useful for  
 CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
 CC or treating tumours. The present DNA sequence represents a SAGE tag that  
 CC was used in the exemplification of the invention.

XX Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 TACAACCTCTG 30

Db 10 TACAACCTCTG 1

RESULT 257

AEC05483

ID AEC05483 standard; DNA; 11 BP.

XX AC AEC05483;

XX 20-OCT-2005 (first entry)

DE Factor VII mutant nucleic acid gene analysis probe, SEQ ID 2.

XX analysis; SNP detection; factor VII; probe; ss.

XX Synthetic.

XX JP2005218310-A.

XX 18-AUG-2005.

XX 03-FEB-2004; 2004JP-00026821.

XX 03-FEB-2004; 2004JP-00026821.

XX (DOKU-) DOKURITSU GYOSHI HOJIN BUSSHITSU ZAIRYO.

XX Miyahara Y, Sakata T;

XX WPI; 2005-575324/59.

XX Device for gene analysis e.g. gene polymorphism analysis, comprises  
 PT insulation film substance immobilized with nucleic acid probe specific  
 PT for target, semiconductor substrate and reference electrode.

XX Example 1; SEQ ID NO 2; 22pp; Japanese.

XX The invention relates to a novel device for gene analysis. The device  
 CC comprises an insulation film substance, a semiconductor substrate and a  
 CC reference electrode. The insulation film substance is immobilized on one  
 CC side with a nucleic acid probe and contacted with a sample solution  
 CC comprising a target gene, and the other side of the surface of insulation  
 CC film substance is contacted with the semiconductor substrate, and the  
 CC reference electrode is in the sample solution. The novel device is  
 CC preferably useful for analyzing a gene polymorphism. The device enables  
 CC rapid, cost effective, highly sensitive and accurate gene analysis. This  
 CC oligo represents a factor VII mutant nucleic acid probe used in the gene  
 CC analysis of the invention.

XX Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 GTCCTCTGAG 42

Db 2 GTCCTCTGAG 11

RESULT 258

AAQ24028/C

ID AAQ24028 standard; DNA; 12 BP.

XX AC AAQ24028;

XX 25-MAR-2003 (revised)

DT 21-SEP-1992 (first entry)

XX Herpesvirus inhibiting antisense oligonucleotide.

XX HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster;

XX Epstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.

XX Synthetic.

XX WO9205284-A.

XX 02-APR-1992.

XX 18-SEP-1991; 91WO-US006646.

XX 21-SEP-1990; 90US-00586185.

XX (UYMA-) UNIV MARYLAND BALTIMORE.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Aurelian L, Tso P;

XX WPI; 1992-132145/16.

XX New anti-sense oligo:nucleotide(s) for inhibiting HSV - also used for  
 PT diagnosis and for inhibiting HIV activation by herpes virus.

XX Claim 1; Page 38; 77pp; English.

XX The sequence is that of an antisense oligonucleotide which can be used  
 CC for inhibiting growth or replication of herpesviruses. It corresponds to  
 CC an antisense sequence of a herpesvirus site, pref. in a gene that is  
 CC essential for synthesising nucleic acids e.g. the immediate early genes  
 CC or Vmw65. It can be prep'd. by solid phase triester or phosphor- amide  
 CC chemistry or by recombinant DNA techniques. It can be used for treating  
 CC infection by herpesviruses, e.g. herpes simplex type 1 (HSV-1) and type 2  
 CC (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cytomegalovirus  
 CC (CMV), human herpesvirus 6 (HHV-6) and 7 (HHV-7). In addition, the  
 CC inhibition of herpesvirus growth or replication may indirectly forestall  
 CC the progression of events from HIV exposure to the clinical manifestation  
 CC of AIDS. It may also be useful in the detection, diagnosis and  
 CC manipulation of herpes virus. See also AAQ23764-Q23788 and AAQ24014-  
 CC Q24044. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 12 BP; 3 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 GAGTCTCTCTG 40

Db 12 GAGTCTCTCTG 3

```

RESULT 259
ABH77995
ID ABH77995 standard; DNA; 12 BP.
XX AC
XX ABH77995;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 277988 for detecting SNP TSC0005414.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 277988; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABP00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 13.0%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 20 ATCAACTCT 29
XX Db 1 ATCAACTCT 10
XX
XX RESULT 260
ABH77995
ID ABH77995 standard; DNA; 12 BP.
XX AC
XX ABH77995;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 277988 for detecting SNP TSC0005414.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 277988; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABP00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 13.0%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 20 ATCAACTCT 29
XX Db 1 ATCAACTCT 10
XX
XX RESULT 260
ABH77995
ID ABH77995 standard; DNA; 12 BP.
XX AC
XX ABH77995;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 277988 for detecting SNP TSC0005414.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.

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KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 341012; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABP00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 13.0%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 20 ATCAACTCT 29
XX Db 1 ATCAACTCT 10
XX
XX RESULT 261
ABH77995
ID ABH77995 standard; DNA; 12 BP.
XX AC
XX ABH77995;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 367500 for detecting SNP TSC0056379.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.

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XX PI Olek A, Piepenbrock C, Berlin K;  
 XX DR WPI; 2001-657177/75.  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 367500; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 13.0%; Score 10; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 43 AGGTAAGAG 52  
 DB 10 AGGTAAGAG 1  
 |||||  
 |||||  
 RESULT 262  
 ABI26778  
 ID ABI26778 standard; DNA; 12 BP.  
 AC ABI26778;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide primer SEQ ID NO 326751 for detecting SNP TSC0033263.  
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 326751; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 13.0%; Score 10; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 20 ATCAACTCT 29  
 DB 3 ATCAACTCT 12  
 |||||  
 |||||  
 RESULT 263  
 ABH91915/c  
 ID ABH91915 standard; DNA; 12 BP.  
 AC ABH91915;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide primer SEQ ID NO 291908 for detecting SNP TSC0014997.  
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 291908; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 2 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

```

Query Match      13.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GAGGTAAGA 51
Db 10 GAGGTAAGA 1

RESULT 264
ABI53146/C
ID ABI53146 standard; DNA; 12 BP.
XX AC
XX AC ABI53146;
XX DT
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 353119 for detecting SNP TSC0010241.
XX KW
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200177384-A2.
XX PD
XX PD 18-OCT-2001.
XX PF
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR
XX PR 07-APR-2000; 2000DE-01019173.
XX PA
XX PA (EPIG-) EPIGENOMICS AG.
XX PI
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR
XX DR WPI; 2001-657177/75.
XX PT
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS
XX PS Claim 1; SEQ ID NO 353119; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ
XX SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;

Query Match      13.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATCAACTCT 29
Db 11 ATCAACTCT 2

RESULT 265
ABH81026
ID ABH81026 standard; DNA; 12 BP.
XX AC
XX AC ABH81026
XX DT
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 291907 for detecting SNP TSC0014997.
XX KW
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200177384-A2.

```

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AC ABH81026;
XX DT
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 281019 for detecting SNP TSC0009317.
XX KW
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200177384-A2.
XX PD
XX PD 18-OCT-2001.
XX PF
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR
XX PR 07-APR-2000; 2000DE-01019173.
XX PA
XX PA (EPIG-) EPIGENOMICS AG.
XX PI
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR
XX DR WPI; 2001-657177/75.
XX PT
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS
XX PS Claim 1; SEQ ID NO 281019; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ
XX SQ Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match      13.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GAGGTAAGA 51
Db 1 GAGGTAAGA 10

RESULT 266
ABH91914/C
ID ABH91914 standard; DNA; 12 BP.
XX AC
XX AC ABH91914;
XX DT
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 291907 for detecting SNP TSC0014997.
XX KW
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200177384-A2.

```





```

CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match      13.0%; Score 10; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AGGTAAGAG 52
   |||||
Db 3 AGGTAAGAG 12

RESULT 269
ABI22756/c
ID ABI22756 standard; DNA; 12 BP.
XX
AC ABI22756;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 322729 for detecting SNP TSC0031029.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 322729; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match      13.0%; Score 10; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATACAACTCT 29
   |||||
Db 1 ATACAACTCT 10

RESULT 271
ABI24690/c
ID ABI24690 standard; DNA; 12 BP.
XX
AC ABI24690;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 324663 for detecting SNP TSC0032163.

```

```

Db 11 ATACAACTCT 2
   |||||
RESULT 270
ABI66720
ID ABI66720 standard; DNA; 12 BP.
XX
AC ABI66720;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 366693 for detecting SNP TSC0055920.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 366693; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match      13.0%; Score 10; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATACAACTCT 29
   |||||
Db 1 ATACAACTCT 10

RESULT 271
ABI24690/c
ID ABI24690 standard; DNA; 12 BP.
XX
AC ABI24690;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 324663 for detecting SNP TSC0032163.

```

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 324663; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 13.0%; Score 10; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 20 ATCAACTCT 29  
 Db |||||  
 12 ATCAACTCT 3  
 RESULT 272  
 ABC48256/C  
 ID ABC48256 standard; DNA; 13 BP.  
 XX AC  
 XX ABC48256;  
 XX 21-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 48273 for detecting SNP TSC0013776.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 48273; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;  
 Query Match 13.0%; Score 10; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 20 ATCAACTCT 29  
 Db |||||  
 10 ATCAACTCT 1  
 RESULT 273  
 ABC04048  
 ID ABC04048 standard; DNA; 13 BP.  
 XX AC  
 XX ABC04048;  
 XX 20-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 4039 for detecting SNP TSC0001514.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 4039; 29pp + Sequence Listing; German.

PR 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 48273; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;  
 Query Match 13.0%; Score 10; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 20 ATCAACTCT 29  
 Db |||||  
 10 ATCAACTCT 1  
 RESULT 273  
 ABC04048  
 ID ABC04048 standard; DNA; 13 BP.  
 XX AC  
 XX ABC04048;  
 XX 20-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 4039 for detecting SNP TSC0001514.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 4039; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;  
SQ Query Match 13.0%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GAGGTAAGA 51  
DB 2 GAGGTAAGA 11  
|||||

RESULT 274  
ABF37938  
ID ABF37938 standard; DNA; 13 BP.  
XX AC ABF37938;  
XX DT 21-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 137935 for detecting SNP TSC0034489.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX FN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 137935; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
SQ Query Match 13.0%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GAGGTAAGA 51  
DB 1 GAGGTAAGA 10  
|||||

RESULT 275  
ABC48257  
ID ABC48257 standard; DNA; 13 BP.  
XX AC ABC48257;  
XX DT 21-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 48274 for detecting SNP TSC0013776.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX FN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 48274; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;  
SQ Query Match 13.0%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATCAACTCT 29  
DB 4 ATCAACTCT 13  
|||||

RESULT 276

```

ABC62658
ID ABC62658 standard; DNA; 13 BP.
XX
AC ABC62658;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 62675 for detecting SNP TSC0016605.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PP 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 62675; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
XX
Query Match 13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGAGGTTAAAG 50
Db 3 AGAGGTTAAAG 12
|||||
3 AGAGGTTAAAG 12

RESULT 277
ABF37939/c
ID ABF37939 standard; DNA; 13 BP.
XX
AC ABF37939;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 137936 for detecting SNP TSC0034489.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB000713.
07-APR-2000; 2000DE-01019173.
(EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 137936; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 13 BP; 3 A; 5 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GAGGTTAAGA 51
Db 13 GAGGTTAAGA 4
|||||
13 GAGGTTAAGA 4

RESULT 278
ABF82004
ID ABF82004 standard; DNA; 13 BP.
XX
AC ABF82004;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 182001 for detecting SNP TSC0044987.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PP 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;

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XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 182001; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 6 A; 1 C; 4 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 13.0%; Score 10; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 40 GAGAGGTAA 49  
 Db 3 GAGAGGTAA 12  
 RESULT 279  
 ABH65593  
 ID ABH65593 standard; DNA; 13 BP.  
 XX AC ABH65593;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 265570 for detecting SNP TSC0064365.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 265570; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 1 Other;  
 SQ Query Match 13.0%; Score 10; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 20 ATACAACTCT 29  
 Db 3 ATACAACTCT 12  
 RESULT 280  
 ABC62659/C  
 ID ABC62659 standard; DNA; 13 BP.  
 XX AC ABC62659;  
 XX 21-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 62676 for detecting SNP TSC0016605.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 62676; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 1 A; 6 C; 0 G; 6 T; 0 U; 0 Other;  
 SQ Query Match 13.0%; Score 10; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AGAGGTAAG 50
Db 11 AGAGGTAAG 2

RESULT 281
ABH24089/C
ID ABH24089 standard; DNA; 13 BP.
XX AC ABH24089;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 224066 for detecting SNP TSC0054592.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX DE Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PF Claim 1; SEQ ID NO 224066; 29pp + Sequence Listing; German.
XX PR This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;

Query Match 13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAA 48
Db 11 TGAGAGGTAA 2

RESULT 282
ABC04049/C
ID ABC04049 standard; DNA; 13 BP.
XX AC ABC04049;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 74402 for detecting SNP TSC0019120.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.

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DT 20-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 4040 for detecting SNP TSC0001514.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX DE Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PF Claim 1; SEQ ID NO 4040; 29pp + Sequence Listing; German.
XX PR This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 GAGGTAAGA 51
Db 12 GAGGTAAGA 3

RESULT 283
ABC74385/C
ID ABC74385 standard; DNA; 13 BP.
XX AC ABC74385;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 74402 for detecting SNP TSC0019120.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.

```

PT	methylation status.
XX	
PS	Claim 1; SEQ ID NO 224065; 29pp + Sequence Listing; German.
XX	
CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at <a href="http://ftp.wipo.int/pub/published_pct_sequences">ftp.wipo.int/pub/published_pct_sequences</a>
XX	
SC	Sequence 13 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 1 Other;
	Query Match 13.0%; Score 10; DB 1; Length 13;
	Best Local Similarity 100.0%; Pred. No. 1.5e+02;
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	39 TGAGAGGTAA 48
DB	3 TGAGAGGTAA 12
RESULT 285	
ABC74384	
ID	ABC74384 standard; DNA; 13 BP.
XX	
AC	ABC74384;
XX	
DT	21-FEB-2002 (first entry)
XX	
DE	Oligonucleotide SEQ ID NO 74401 for detecting SNP TSC0019120.
XX	
KW	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS	Homo sapiens.
XX	
FN	WO200177384-A2.
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-IB000713.
XX	
PR	07-APR-2000; 2000DE-01019173.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K;
XX	
DR	WPI; 2001-657177/75.
XX	
PT	Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
PT	
XX	
PS	Claim 1; SEQ ID NO 74401; 29pp + Sequence Listing; German.
XX	
CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence



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CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match      13.0%; Score 10; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAA 48
Db 4 TGAGAGGTAA 13

RESULT 286
ABH65592/c
ID ABH65592 standard; DNA; 13 BP.
XX
XX AC ABH65592;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 265569 for detecting SNP TSC0064365.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 265569; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 1 Other;

  Query Match      13.0%; Score 10; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATACAACCTCT 29
Db 11 ATACAACCTCT 2

data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences

  Query Match      13.0%; Score 10; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GAGAGGTAAA 49
Db 11 GAGAGGTAAA 2

RESULT 288
ADQ58875/c
ID ADQ58875 standard; DNA; 13 BP.
XX
XX AC ADQ58875;
XX
XX 23-SEP-2004 (first entry)
XX
XX Yin yang-1 potential splice variant acceptor site #5.
XX
XX antidiabetic; immunosuppressive; cytostatic; Yin Yang-1;

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RESULT 287
ABF82005/c
ID ABF82005 standard; DNA; 13 BP.
XX
XX AC ABF82005;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 182002 for detecting SNP TSC0044987.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 182002; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 4 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match      13.0%; Score 10; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GAGAGGTAAA 49
Db 11 GAGAGGTAAA 2

RESULT 288
ADQ58875/c
ID ADQ58875 standard; DNA; 13 BP.
XX
XX AC ADQ58875;
XX
XX 23-SEP-2004 (first entry)
XX
XX Yin yang-1 potential splice variant acceptor site #5.
XX
XX antidiabetic; immunosuppressive; cytostatic; Yin Yang-1;

```

KW transcription factor; type 1 diabetes; transgenic; diabetes;  
 KW multifunctional transcription factor; type 2 diabetes;  
 KW autoimmune disease; cancer; mineral metabolism disorder;  
 KW lipid metabolism disorder; rat; YY-1; splice variant; acceptor site; ds.  
 OS Rattus norvegicus.  
 XX  
 XX WO2004056857-A2.  
 XX  
 XX 08-JUL-2004.  
 XX  
 XX 19-DEC-2003; 2003WO-EP014762.  
 XX  
 XX 20-DEC-2002; 2002DE-01061650.  
 XX  
 XX (UYGR ) UNIV GREIFSWALD.  
 XX  
 XX KJoeting I, KJoeting N;  
 XX  
 XX WPI; 2004-507695/48.  
 XX  
 XX New variant of the Yin Yang-1 transcription factor, useful for treating  
 PT e.g. diabetes and autoimmune disease, also for diagnosing predisposition  
 PT and in screening for therapeutic agents.  
 XX  
 XX Disclosure; Page 62; 193pp; German.  
 XX  
 CC The invention describes a protein variant of the Yin Yang-1 transcription  
 CC factor (I), having a 411 amino acid (aa) sequence (4) reproduced. Also  
 CC described are: protein (Ia) that is a homologue of (4) and includes Arg a  
 CC position 303 and Lys at position 311; peptide (II) that is a fragment of  
 CC (I) or (Ia) and includes the positions 303 and 311 of (4); nucleic acid  
 CC (III) that encodes (I), (Ia) or (II); an antibody (Ab) directed against  
 CC (I) or (Ia); methods for determining a tendency to develop type 1  
 CC diabetes; transgenic non-human mammal (A) in which the germ and somatic  
 CC cells contain a nucleic acid (or segment) encoding a 411 aa sequence (2),  
 CC or sequences with at least 95, best 99% homology, where the homologue  
 CC includes 303Met and 311Arg; and use of (A) to screen for compounds (B)  
 CC that are protective against diabetes. The methods are useful for  
 CC modulating activity of the YY1 (Yin Yang-1) multifunctional transcription  
 CC factor. (I), or its homologues and peptides, also nucleic acids encoding  
 CC them and antisense oligonucleotides, are useful for treatment of type 1  
 CC and 2 diabetes, autoimmune diseases, cancer and disorders of mineral and  
 CC lipid metabolism. Detecting mutations in the human analogue of (4) is  
 CC used to determine a predisposition for these diseases. Transgenic animals  
 CC that contain the sequence encoding (4), or its homologues, are used to  
 CC screen for agents protective against diabetes. This sequence represents a  
 CC potential splice acceptor site for splice variants of Yin yang-1  
 CC transcription factor.  
 XX  
 XX Sequence 13 BP; 3 A; 7 C; 1 G; 2 T; 0 U; 0 Other;  
 QY Query Match 13.0%; Score 10; DB 1; Length 13;  
 DB Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 37 TCTGAGAGGT 46  
 DB 10 TCTGAGAGGT 1  
 RESULT 289  
 AAT10984/C  
 ID AAT10984 standard; DNA; 14 BP.  
 XX  
 XX AAT10984;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 19-JUN-1996 (first entry)  
 XX  
 XX H.influenzae detection probe binds to 16S rRNA gene at pos. 1255-69.  
 DE  
 XX Probe; Haemophilus influenzae; 16S rRNA gene; E.coli; helper probe;  
 KW

KW acridinium ester label; H.aphrophilus; H.ducrei; H.haemolyticus;  
 KW H.parahaemolyticus; H.parainfluenzae; H.paraphrophilus; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX US5472843-A.  
 XX  
 XX 05-DEC-1995.  
 XX  
 XX 01-APR-1994; 94US-00221968.  
 XX  
 XX 25-APR-1991; 91US-00690788.  
 XX  
 XX (GENP-) GEN-PROBE INC.  
 XX  
 XX Milliman CL;  
 XX  
 XX WPI; 1996-029808/03.  
 XX  
 XX Detection of Haemophilus influenzae nucleic acid - using new  
 PT oligo:nucleotide probes.  
 XX  
 XX Example 1; Col 9; 9pp; English.  
 XX  
 CC Probes AAT10983-4 are used for the specific detection of Haemophilus  
 CC influenzae. They bind to a region of the H.influenzae 16S rRNA gene at a  
 CC pos. corresp. to bases 837-854 or 1255-69 of the E.coli 16S rRNA gene.  
 CC The probes can also be used in the detection by the helper probes  
 CC AAT10985-9. The probes are pref. labelled with an acridinium ester label.  
 CC The probes are specific for H.influenzae and do not bind to nucleic acids  
 CC from H.aphrophilus, H.ducrei, H.haemolyticus, H.parahaemolyticus,  
 CC H.parainfluenzae or H.paraphrophilus. (Updated on 25-MAR-2003 to correct  
 CC PF field.)  
 XX  
 XX Sequence 14 BP; 1 A; 6 C; 3 G; 4 T; 0 U; 0 Other;  
 QY Query Match 13.0%; Score 10; DB 1; Length 14;  
 DB Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 55 AGCGAAGCTG 64  
 DB 12 AGCGAAGCTG 3  
 RESULT 290  
 AAV99057/C  
 ID AAV99057 standard; RNA; 14 BP.  
 XX  
 XX AAV99057;  
 XX  
 XX 17-MAR-1999 (first entry)  
 DT  
 XX  
 XX Human EGF-R target sequence nucleotide position 3489.  
 DE  
 XX  
 XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;  
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;  
 KW cancer; genetic drift; detection; mutation; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9833893-A2.  
 XX  
 XX 06-AUG-1998.  
 XX  
 XX 14-JAN-1998; 98WO-US000730.  
 XX  
 XX 31-JAN-1997; 97US-0036476P.  
 PR 04-DEC-1997; 97US-00985162.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX (UYAS-) UNIV ASTON.  
 XX

PI Akhtar S, Fell P, Mcswiggen JA;  
 DR WPI, 1998-437449/37.  
 XX  
 XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal  
 PT growth factor receptor, useful for inhibiting cell proliferation and for  
 PT treating cancers.  
 XX  
 PS Claim 6; Page 89; 109pp; English.  
 XX  
 CC The present invention describes enzymatic nucleic acid molecules (NAMS)  
 CC which specifically cleave RNA derived from an epidermal growth factor  
 CC receptor (EGF-R) gene. AA97221 to AA98043 and AA98979 to AA99090  
 CC represent specifically claimed target sequence from human EGF-R. AA98044  
 CC to AA98866 and AA98867 to V9878 represent hammerhead ribozymes and  
 CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for  
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGF-R  
 CC expression levels e.g. to inhibit cell proliferation in the prevention or  
 CC treatment of cancers. The NAMS can also be used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of EGF-R RNA in a cell  
 XX  
 SQ Sequence 14 BP; 0 A; 6 C; 5 G; 0 T; 3 U; 0 Other;  
 Query Match 13.0%; Score 10; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 49 AGAGCCAGCG 58  
 DB |||||  
 14 AGAGCCAGCG 5  
 RESULT 291  
 AA67150/c  
 ID AA67150 standard; DNA; 14 BP.  
 XX  
 AC AA67150;  
 XX  
 DT 11-JAN-1999 (first entry)  
 DE Haemophilus influenzae 16S rRNA probe #1.  
 XX  
 KW Haemophilus influenzae; 16S rRNA; probe; hybridisation; identification;  
 KW bacterial colony; ribosomal RNA; ss.  
 XX  
 OS Synthetic.  
 OS Haemophilus influenzae.  
 XX  
 PN US5830654-A.  
 XX  
 PD 03-NOV-1998.  
 XX  
 PF 04-DEC-1995; 95US-00567196.  
 XX  
 PR 25-APR-1991; 91US-00690788.  
 PR 01-APR-1994; 94US-00221968.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Millman CL;  
 XX  
 DR WPI, 1998-609234/51.  
 XX  
 PT Nucleic acid hybridisation probe specific for Haemophilus influenzae -  
 PT useful for identification of H. influenzae, optionally used with helper  
 PT probes.  
 XX  
 PS Claim 1; Col 13; 10pp; English.  
 XX  
 CC The present sequence represents a nucleic acid hybridisation probe that  
 CC hybridises to Haemophilus influenzae rRNA in a region corresponding to  
 CC nucleotides 1255-1268 of E. coli 16S rRNA. The probe can be labelled,

CC especially with an acridinium ester, and used in an assay for H.  
 CC influenzae, optionally together one or more helper probes. The probe does  
 CC not hybridise to nucleic acids from H. aphrophilus, H. ducreyi, H.  
 CC parainfluenzae, H. parahaemolyticus, H. parainfluenzae or H.  
 CC parainfluenzae. The probe enables rapid, non-subjective identification  
 CC of the presence of specific ribosomal RNA sequences that are unique to  
 CC all serotypes and bio-types of H. influenzae  
 XX  
 SQ Sequence 14 BP; 1 A; 6 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 13.0%; Score 10; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 55 AGCGAAGCTG 64  
 DB |||||  
 12 AGCGAAGCTG 3  
 RESULT 292  
 AA67165/c  
 ID AA67165 standard; RNA; 14 BP.  
 XX  
 AC AA67165;  
 XX  
 DT 19-JUN-2000 (first entry)  
 DE Aryl hydrocarbon nuclear transport target site SEQ ID NO:891.  
 XX  
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;  
 KW ophthalmologic; anti-inflammatory; antiarthritic; antipsoriatic; ARMD;  
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
 KW age related macular degeneration; inflammation; neovascular glaucoma;  
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tuberculous sclerosis; pot-wine stain; Sturge Weber syndrome;  
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09950403-A2.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 24-MAR-1999; 99WO-US006507.  
 XX  
 PR 27-MAR-1998; 98US-0079678P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;  
 XX  
 DR WPI, 1999-591315/50.  
 XX  
 PT Novel ribozymes for modulating the synthesis, expression and/or stability  
 PT of an mRNA encoding an angiogenic factors.  
 XX  
 PS Claim 53; Page 90; 305pp; English.  
 XX  
 CC The present invention describes enzymatic nucleic acid molecules with RNA  
 CC cleaving activity, which specifically cleave RNA encoded by an aryl  
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA6775 to  
 CC AA67167 and AA67561 to AA67622 represent ribozyme sequences for ARNT,  
 CC and AA67168 to AA67560 and AA67623 to AA67684 represent their  
 CC corresponding target sequences; AA67685 to AA67835 and AA67987 to  
 CC AA679154 represent ribozyme sequences for Tie-2, and AA67836 to AA679086  
 CC and AA679155 to AA679222 represent their corresponding target sequences;  
 CC AA679223 to AA679361 and AA679501 to AA679595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AA679362 to AA679500 and  
 CC AA679596 to AA679688 represent their corresponding target sequences;  
 CC AA679689 to AA679745 and AA679746 to AA679747 represent ribozyme sequence

CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
 CC AAA23422 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or  
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
 CC integrin subunit beta-3, integrin subunit alpha-6, or tie-2. They are  
 CC especially used to treat cancer, diabetic retinopathy, age related  
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tubercous sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3  
 XX  
 SQ Sequence 14 BP; 3 A; 5 C; 2 G; 0 T; 4 U; 0 Other;  
 Query Match 13.0%; Score 10; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 58 GAAGCTGATG 67  
 Db |||||  
 10 GAAGCTGATG 1  
 RESULT 293  
 ID AAN92945/c  
 XX AAN92945 standard; DNA; 12 BP.  
 AC AAN92945;  
 XX  
 DT 01-JUL-1990 (first entry)  
 DE Consensus sequence for mammalian expression vector.  
 XX  
 KW Murine autonomously replicating sequence; consensus sequence;  
 KW mammalian expression vector.  
 XX  
 OS Mouse.  
 XX  
 PN EP306848-A.  
 XX  
 PD 15-MAR-1989.  
 XX  
 PF 02-SEP-1988; 88EP-00114317.  
 XX  
 PR 09-SEP-1987; 87DE-03730246.  
 XX  
 PA (BOE ) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Grummt F, Weidle U;  
 XX  
 DR WPI; 1989-078357/11.  
 XX  
 PT Expression vectors for mammalian cells - with two consensus sequences and  
 PT inefficient selection system.  
 XX  
 PS Claim 2; Page 8; 12pp; German.  
 XX  
 CC The inventors claim vectors for the expression of heterologous proteins  
 CC in mammalian cells. Each vector has a first and second consensus sequence  
 CC (CS). The CS or their homologues are present in known murine autonomously  
 CC replicating sequences (MuARS). The first CS is homologous to AAN92945.  
 CC The inefficient selection system comprises the tk gene and a truncated tk  
 CC promoter. The vectors also contain a gene coding for a protein and the  
 CC necessary promoter and terminator sequences for the expression of this  
 CC gene. The expression vectors provide rapid amplification, allow selection  
 CC of best clones in a short time, are of universal utility in mammalian  
 CC cells, and are free of viral origin sequences  
 XX  
 SQ Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 12.2%; Score 9.4; DB 1; Length 12;  
 Best Local Similarity 90.9%; Pred. No. 1.6e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 34 TCCTCTGAGAG 44  
 Db |||||  
 11 TCCTCTGAGAG 1  
 RESULT 294  
 ID ACC46925 standard; DNA; 20 BP.  
 XX AC ACC46925;  
 XX  
 DT 05-JUN-2003 (first entry)  
 DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:22.  
 XX  
 KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;  
 KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;  
 KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;  
 KW psoriasis; diabetes; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate backbone"  
 FT modified\_base 1..5  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"  
 FT modified\_base 16..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"  
 XX  
 PN WO200297133-A1.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 21-MAY-2002; 2002WO-US016135.  
 XX  
 PR 25-MAY-2001; 2001US-00865866.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Wyatt JR;  
 XX  
 DR WPI; 2003-140495/13.  
 XX  
 PT New compound that hybridizes with and inhibits the expression of  
 PT Phospholipase A2, group IIA, useful for preparing a composition for  
 PT treating or preventing inflammation, cancer, psoriasis or diabetes.  
 XX  
 PS Claim 3; Page 86; 135pp; English.  
 XX  
 CC The present invention describes a compound (I) comprising 8-50  
 CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,  
 CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase  
 CC A2, group IIA (synovial), where the compound specifically hybridises with  
 CC and inhibits the expression of phospholipase A2, group IIA (synovial).  
 CC Also described: (1) a composition comprising the compound and a carrier  
 CC or diluent; (2) a method of inhibiting the expression of phospholipase  
 CC A2, group IIA in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with phospholipase A2, group IIA  
 CC (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and  
 CC antipsoriatic activities, and can be used in vaccines and in gene  
 CC treating or preventing inflammation, cancer, psoriasis or diabetes. The  
 CC present sequence represents a human phospholipase A2 group IIA (synovial)

CC chimeric phosphorothioate antisense oligonucleotide, which is used in an  
 CC example from the present invention  
 XX  
 SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;  
 Query Match 12.2%; Score 9.4; DB 1; Length 20;  
 Best Local Similarity 90.9%; Pred. No. 2.4e+02;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 35 CCTCTGAGAGG 45  
 Db 8 CCTCTGAGAGG 18  
 |||||  
 |||||

RESULT 295  
 ID AAZ64698 standard; RNA; 14 BP.  
 XX  
 AC AAZ64698;  
 XX  
 DT 28-MAR-2000 (first entry)  
 XX  
 DE Substrate for hairpin ribozyme which cleaves HCV at nt. 886.  
 XX  
 KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;  
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;  
 KW autoimmune disease; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO9955847-A2.  
 XX  
 PD 04-NOV-1999.  
 XX  
 XX 26-APR-1999; 99WO-US009027.  
 XX  
 XX 27-APR-1998; 98US-0083217P.  
 PR 18-SEP-1998; 98US-0100842P.  
 PR 25-FEB-1999; 99US-00257608.  
 PR 23-MAR-1999; 99US-00274553.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejak D;  
 XX  
 DR WPI; 2000-062023/05.  
 XX  
 PT Novel ribozymes for the treatment of diseases and conditions related to  
 PT hepatitis C infection.  
 XX  
 PS Claim 2; Page 94; 123pp; English.  
 XX  
 CC The present sequence represents the preferred target sequence of an  
 CC enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the  
 CC Hepatitis C virus (HCV) RNA sequence at the base position given in the  
 CC descriptor line. The HCV sequence was screened for optimal ribozyme  
 CC target sites using a computer folding algorithm and regions of the mRNA  
 CC which did not form secondary folding structures and contained potential  
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to  
 CC target these sites and their activities optimised by either varying the  
 CC length of the binding arms or by modification to prevent degradation by  
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or  
 CC viral replication, and are used to treat diseases associated with  
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and  
 CC hepatocellular carcinoma. The ribozymes may be used in combination with  
 CC interferon to treat HCV infection, other infectious diseases, autoimmune  
 CC diseases, and cancer  
 XX  
 SQ Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;  
 Query Match 11.4%; Score 8.8; DB 1; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAACAGACGCGC 13  
 |||||  
 Db 14 AAACAGGACGAC 3  
 |||||

RESULT 296  
 ABX01535/c  
 ID ABX01535 standard; RNA; 14 BP.  
 XX  
 AC ABX01535;  
 XX  
 DT 23-DEC-2002 (first entry)  
 XX  
 DE Hepatitis C virus substrate #20 for HCV hairpin ribozyme #20.  
 XX  
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virolicide;  
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
 KW type I interferon; interferon alpha; interferon beta; cytostatic;  
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;  
 KW substrate; hairpin ribozyme; HP ribozyme; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US2002082225-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 XX 23-MAR-1999; 99US-00274553.  
 XX  
 PR 23-MAR-1999; 99US-00274553.  
 XX  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (ROBE/) ROBERTS B.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;  
 XX  
 DR WPI; 2002-617759/66.  
 XX  
 PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral  
 PT replication and are useful to treat hepatitis C virus infections and  
 PT cirrhosis, liver failure or hepatocellular carcinoma.  
 XX  
 PS Claim 2; Page 59; 80pp; English.  
 XX  
 CC The present invention relates to enzymatic nucleic acids which  
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin  
 CC (HP) motif where the binding arms comprise sequences complementary to one  
 CC of the substrate sequences defined in the specification. The HCV  
 CC ribozymes are useful for modulating the expression and/or replication of  
 CC HCV. They can be used to treat cirrhosis, liver failure and/or  
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating  
 CC a condition associated with HCV infection in conjunction with one or more  
 CC other drug therapies, particularly type I interferon, especially  
 CC interferon alpha, beta or gamma or consensus interferon. The present  
 CC sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note:  
 CC Some of the sequence data for this patent did not form part of the  
 CC printed specification. The complete sequence data for this patent was  
 CC obtained in electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipspDIDEntry.html  
 XX  
 SQ Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;  
 Query Match 11.4%; Score 8.8; DB 1; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAACAGACGCGC 13

```

Db      14 AAACAGCAGCAGC 3
||||| ||| ||
RESULT 297
AEB76459/c
ID AEB76459 standard; RNA; 14 BP.
XX
AC AEB76459;
XX
XX
DT 22-SEP-2005 (first entry)
XX
DE Hepatitis C virus hairpin ribozyme substrate sequence.
XX
XX ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
XX antiviral; gene therapy; substrate; ss.
XX
OS Hepatitis C virus.
XX
XX US2002013458-A1.
XX
XX 31-JAN-2002.
XX
XX 15-FEB-2000; 2000US-00504231.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX (BLATT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX (ROBE/) ROBERTS E.
XX (PAVO/) PAVO P A.
XX (MACE/) MACEJACK D.
XX
XX Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;
XX WPI; 2002-215899/27.
XX
XX New enzymatic nucleic acid molecule, which specifically cleaves minus
XX strand RNA derived from hepatitis C virus, useful for modulating the
XX expression and/or replication of hepatitis C virus.
XX
XX Example 1; Page 43; 65pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule which
XX specifically cleaves minus strand RNA derived from hepatitis C virus
XX (HCV). The binding arms of the molecule comprise ribozyme sequences. The
XX molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
XX Zinzyme motifs. Also described: (1) a pharmaceutical composition
XX comprising the novel enzymatic nucleic acid; (2) a mammalian cell
XX including the novel enzymatic nucleic acid; (3) an expression vector
XX comprising a nucleic acid sequence encoding at least one enzymatic
XX nucleic acid molecule, in a manner, which allows expression of that
XX molecule; (4) a mammalian cell including an expression vector of (3); (5)
XX methods for treating cirrhosis, liver failure or hepatocellular carcinoma
XX by administering to a patient the novel enzymatic nucleic acid or the
XX vector of (3); (6) a method of treating a patient having a condition
XX associated with HCV infection, by contacting cells of the patient with
XX the nucleic acid molecule, and further employing one or more drug
XX therapies; (7) a method for inhibiting HCV replication in a mammalian
XX cell by administering the novel enzymatic nucleic acid; and (8) a method
XX of cleaving a separate RNA molecule by contacting the novel enzymatic
XX nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
XX is useful for modulating the expression and/or replication of hepatitis C
XX virus (HCV), and for inhibiting the expression of HCV minus strand. The
XX nucleic acid may also be used to treat or prevent the occurrence of a
XX disease state in a patient. The present sequence represents an HCV
XX hairpin ribozyme target substrate sequence which is used in the
XX exemplification of the present invention.
XX
XX Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
Query Match 11.4%; Score 8.8; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Indels 0; Gaps 0;

Db      2 AAACAGCAGCAGC 13
||||| ||| ||
Db      14 AAACAGCAGCAGC 3
||||| ||| ||
RESULT 298
AEB19896
ID AEB19896 standard; DNA; 15 BP.
XX
AC AEB19896;
XX
XX 25-AUG-2005 (first entry)
XX
DE PCR primer #1.
XX
XX Microorganism detection; PCR; primer; intestine infection;
XX gastrointestinal-gen.; gastrointestinal disease; infection; ss.
XX
XX Vibrio fluvialis.
XX
XX CN1560273-A.
XX
XX 05-JAN-2005.
XX
XX 26-FEB-2004; 2004CN-00015461.
XX
XX 26-FEB-2004; 2004CN-00015461.
XX
XX (UYZH-) UNIV ZHONGSHAN.
XX
XX Deng X, He J, Wang Z;
XX WPI; 2005-296834/31.
XX
XX Kit for diagnosing gene of pathogenic bacterial and river vibron of
XX aquatic animal and human and testing method thereof.
XX
XX Claim 1; Page 2; 7pp; Chinese.
XX
XX The invention relates to a kit for detecting aquatic animal pathogens and
XX human pathogens, comprising a pair of PCR primers used to detect specific
XX DNA fragments of Vibrio fluvialis. The kit and method can be used in
XX bacteria tracking and detection of aquatic animal pathogens in the course
XX of breeding and also in the clinical detection of human intestinal acute
XX infections, as well as in environmental monitoring. This sequence
XX represents a PCR primer used in the scope of the invention.
XX
XX Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 11.4%; Score 8.8; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Indels 0; Gaps 0;

Db      34 TCCTCTGAGAGG 45
||||| ||| |||
Db      3 TCCTCCGAGG 14
||||| ||| |||
RESULT 299
ACF57644
ID ACF57644 standard; DNA; 10 BP.
XX
AC ACF57644;
XX
XX 22-APR-2004 (first entry)
XX
XX Human ALDOB gene allele-specific primer SEQ ID NO: 95.
XX
XX Human; ALDOB; fructose-bisphosphate aldolase B; SNP;
XX single nucleotide polymorphism; primer; probe; ss.
XX

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OS Homo sapiens.
XX WO2003091454-A1.
XX
XX
XX
XX 06-NOV-2003.
XX
XX 26-APR-2002; 2002WO-US013328.
XX
XX 26-APR-2002; 2002WO-US013328.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Chew A, Kazemi A, Koshiy B;
XX
XX WPI; 2003-877338/81.
XX
XX Claim 41; Page 15; Opp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX fructose-bisphosphate aldolase B (ALDOB) and single nucleotide
XX polymorphisms (SNPs) which have been identified in each sequence. The
XX method of haplotyping the sequences is useful for haplotyping the
XX fructose-bisphosphate aldolase B (ALDOB) gene of an individual or for
XX validating the ALDOB protein as a candidate target for treating a medical
XX condition predicted to be associated with ALDOB activity. The present
XX sequence is an allele-specific primer/probe used to identify the
XX haplotype of the human ALDOB gene in the exemplification of the invention
XX
XX Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 10.9%; Score 8.4; DB 1; Length 10;
XX Best Local Similarity 90.0%; Pred. No. 1.9e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 35 CCTCTGAGAG 44
XX |||||
XX Db 1 CCTCTGAGAG 10
XX
XX Search completed: April 19, 2006, 16:12:08
XX Job time : 0.001 secs
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